

atgtggg	cgg agcttaa	agc cctggcc	gcc tgcaggg	gcg gccgcgt	gca ccgggcag	ca 1020
gacccct	tgg cggggct	aaa ggacct	caag gaggtcc	ggg gcctcct	cgc caaggac	ctc 1080
gccgtct	tgg cctcgag	gga ggggct	agac ctctgt	cccc gggacg	accc catgct	cctc 1140
gcctac	cctcc tggacc	cctt gaacac	cacc cccgag	gggg tggcgc	ggcg ctacg	gggg 1200
gagtgg	acgg aggacg	ccgc ccaccg	ggcc ctctct	cgg agagg	ctca tcgga	acctc 1260
cttaag	cgaac agcag	gggg ggaaga	gctc ctttgg	ctct accacg	aggt ggaaa	agccc 1320
ctctccc	ggg tcctgg	ccca tatgg	aggcc accggg	gtac ggcggg	acgt ggctac	cctt 1380
caggccc	ttt ccctgg	agct tgcgg	aggag atccgc	ccgc tcgagg	agga ggtctt	ccgc 1440
ttggcgg	ggcc acccct	tcaa cctca	actcc cgggac	cagc tggaa	aggg gctctt	tgac 1500
gagctta	ggc ttccgc	cctt gaaga	agac aagaag	acag gcaagc	gctc caccag	cgcc 1560
gcggtg	ctgg aggcc	ctac ggagg	ccca cccat	cgtgg agaag	atcct ccagc	accgg 1620
gagctca	ccca agctc	aagaa caccta	cgtg gacccc	cctcc caagc	ctcgt ccaccc	gagg 1680
acgggcc	cgcc tccac	acccg cttca	accag acggcc	acag ccacg	gggag gcttag	tagc 1740
tcggac	ccca acctg	cagaa catccc	cgtc cgcac	cccc tgggc	cagag gatccg	ccgg 1800
gccttc	gtgg ccgagg	ggg ttggg	cgttg gtggc	ccttg actat	agcca gataga	gctc 1860
cgcgct	cctcg cccac	ctct cgggg	acgaa aacct	gatca gggct	cttcca ggagg	ggaag 1920
gacatcc	acaa cccag	accgc aagct	ggatg ttcgg	cgtcc ccccg	agggc cgtgg	acccc 1980
ctgatgc	cgcc gggcg	gcaaa gacgg	tgaac ttcgg	cgtcc tctac	ggcat gtccg	cccat 2040
aggctct	cccc aggag	cttgc catccc	ctac gaggag	gcgg tggc	cctttat agagc	gctac 2100
ttccaa	agct tcccc	aaggt gcggg	ccttg atag	aaaaga ccctg	gagga gggg	aggaag 2160
cggggc	tacg tggaa	accct cttcg	gaaga aggcg	ctac tgccc	gacct caacg	ccccg 2220
gtgaag	agcg tcagg	gaggc cgcgg	agcgc atggc	cttca acatg	cccgt ccagg	gcacc 2280
gccgcc	gacc tcatg	aagct cgccat	ggtg aagct	cttcc cccgc	cctccg ggagat	gggg 2340
gcccgc	atgc tcctc	aggt cgcca	acgag ctctc	cttg agggc	ccccca agcgc	ggggc 2400
gaggagg	tgg cggct	tttgg caagg	aggcc atgg	agaagg cctat	ccccct cgccg	tgccc 2460
ctggagg	tgg aggtg	gggg gat	ggggg aggg	ac tggct	tttccg ccaagg	gt 2508

<210> 408

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 408

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	
1				5					10					15		
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	
			20					25					30			
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	
		35					40					45				
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	
	50					55					60					
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	
65					70					75					80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	
				85					90					95		
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	
			100					105					110			
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	
		115					120					125				
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	
	130					135					140					
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	
145					150				155						160	
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	
				165					170					175		
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	
			180					185					190			
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	
		195					200					205				
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	
	210					215					220					
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	
225					230					235					240	
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	
				245					250					255		
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	
		260						265					270			
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	
		275					280						285			

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
290 295 300
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305 310 315 320
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
325 330 335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
340 345 350
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
355 360 365
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
370 375 380
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385 390 395 400
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
405 410 415
His Arg Asn Leu Leu Lys Arg Asn Glu Gly Lys Glu Lys Leu Leu Trp
420 425 430
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
435 440 445
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
450 455 460
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465 470 475 480
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
485 490 495
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
500 505 510
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
515 520 525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
530 535 540
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545 550 555 560
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
565 570 575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
580 585 590
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
595 600 605
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 409

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 409

atgaattccg aggcgatgct tccgctcttt gaaccctaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaagccc cctccttcgc ccacgaggcc	240

tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctggggg ttaccgcgc tcgagggtccc cggctacgag	360
gcgggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgagggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcggtgggg gacccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctctggagg cccccgccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccc ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gcgcggtgca ccgggcagca	1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctcggtgccg gggacgacct catgctcctc	1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg	1200
gagtggacgg aggacgcgc ccaccgggc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgt tcgaggggga ggagaagctc ctttgccct accacgaggt ggaaaagccc	1320
ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccttgagct tgcggaggag atccgcgcc tcgaggagga ggtcttcgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaaggg gctctttgac	1500
gagcttaggc ttccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggcctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg	1680
acgggcgcgc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgaccca acctgcagaa catccccgtc cgcacccct tgggcccagag gatccgcgg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgctcctc cccacctctc cggggacgaa aacctgatca gggcttcca ggaggggaag	1920
gacatccaca cccagaccgc aagctggatg ttcggcgctc ccccgaggc cgtggacccc	1980
ctgatgcgc gggcgccaa gacggtgaac ttcggcgctc tctacggcat gtccgcccat	2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100

ttccaaagct tccccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
 cggggctacg tggaaccct cttcggaaga aggcgctacg tgcccacact caacgcccgg 2220
 gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gcccgcatgc tcctccaggt cgccaacgag ctctccttgg agggccccca agcgcgggcc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt 2508

<210> 410

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 410

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Phe Glu Gly Glu Glu Lys Leu Leu Cys
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 411

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 411

```
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac      60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc      120
gaaccgggtgc aggcgggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac      180
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttcg ccacgaggcc      240
tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc      300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggtacgag      360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc      420
atcctcaccg ccgaccgga cctctaccaa ctctctccg accgcgtcgc cgtcctccac      480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag      540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag      600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc      660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccaactg      720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg      780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttccct ggagaggctg      840
gagttcgga gcctcctcca cgagttcggc ctctggagg ccccgcccc cctggaggag      900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc      960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca     1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc     1080
gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgaccc catgctctc     1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgggcg ctacgggggg     1200
gagtggaagg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc     1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc     1320
ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt     1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttcgc     1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac     1500
```

gagcttaggc ttcccttttt gaagaagacg aagaagacag gcaagcgctc caccagcgcc 1560
gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620
gagctacca agctcaagaa cacctacgtg gacccccctcc caagcctcgt ccacccgagg 1680
acggggccgcc tccacacccg cttcaaccag acggccacgg ccacgggggag gcttagtagc 1740
tccgacccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgccgg 1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
cgcgctcctg cccacctctc cggggacgaa aacctgatca gggctcttcca ggaggggaag 1920
gacatccaca cccagaccgc aagctggatg ttcggcgctc ccccgagggc cgtggacccc 1980
ctgatgcgcc gggcgggccaa gacggtgaac ttcggcgctc tctacggcat gtccgccccat 2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tccccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
cggggctacg tggaaaaccct cttcggaaga aggcgctacg tgcccgacct caacgcccgg 2220
gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcacgc tcctccaggt cgccaacgag ctctccttgg agggccccca agcgcgggcc 2400
gaggagggtg cggttttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggagggtg aggtggggat gggggaggac tggctttccg ccaagggt 2508

<210> 412

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 412

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				

Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	210	215	220	
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	225	230	235	240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	245	250	255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	260	265	270	
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	275	280	285	
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300	
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	305	310	315	320
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val	325	330	335	
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	340	345	350	
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	355	360	365	
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	370	375	380	
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	385	390	395	400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Phe Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 413

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> n

<222> (19)..(21)

<223> n is any base a,t,c, or g.

<400> 413

caggagctta ggcttcccn nttgaagaag acgaagaaga ca

42

<210> 414

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 414

cctaagctcg tcaaagag

18

<210> 415

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 415

```
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac      60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc      120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac      180
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttcgg ccacgaggcc      240
tacgaggcct acaaggcggg gagggccccc acccccaggg acttcccccg gcagctcgcc      300
ctcatcaagg agctggtgga cctcctgggg tttaccggcc tcgagggtccc cggtacgag      360
gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc      420
atcctcaccg ccgaccgcga cctctaccaa ctcgctcccg accgcgtcgc cgtcctccac      480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag      540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag      600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc      660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggccacctg      720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg      780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg      840
gagttcggca gcctcctcca cgagttcggc ctcttgagg cccccgccc cctggaggag      900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc      960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca     1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc     1080
gccgtcttgg cctcgaggga ggggctagac ctcgtgccc gggacgaccc catgctcctc     1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg     1200
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc     1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc     1320
ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt     1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttcgcg     1440
ttggcggggc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac     1500
```

gagcttaggc ttcccgtttt gaagaagacg aagaagacag gcaagcgctc caccagcgcc 1560
gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620
gagctcacca agctcaagaa cacctacgtg gacccccctc caagcctcgt ccacccgagg 1680
acgggcccgc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
tccgacccca acctgcagaa catccccgtc cgcacccccct tgggcccagag gatccgcccg 1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag 1920
gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980
ctgatgcgcc gggcgggcaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040
aggtctctcc aggagcttgc catccccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tccccaaagt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacact caacgcccgg 2220
gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccggt ccagggcacc 2280
gccgcccacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcatgc tcctccaggt cgccaacgag ctctcctcgt agggccccca agcgcggggc 2400
gaggaggtgg cggttttggc caaggaggcc atggagaagg cctatccccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt 2508

<210> 416

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 416

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55				60					
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75				80	

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95
 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Val Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly
835

<210> 417

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 417

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccctcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttcgg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccc acccccaggg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgccg tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgcca cctctaccaa ctcgctcccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcgcca gcctcctcca cgagttcggc ctctggagg cccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tctctcccc ccccgagccc	960

atgtggg	cgg agcttaa	agc cctggcc	gcc tgcaggg	gcg gccgcgt	gca ccgggcag	ca 1020	
gacccct	tgg cggggct	aaa ggacct	caag gaggtcc	ggg gcctcct	cgc caaggac	ctc 1080	
gccgtct	tgg cctcgag	gga ggggct	agac ctctgt	ccc gcccg	gggacgac	ccc catgtct	cctc 1140
gcctac	cctcc tggacc	cctc gaacac	cacc cccgag	gggg tggcg	ggcg ctacg	gggg 1200	
gagtgg	acgg aggac	gcgc ccacc	gggcc ctcct	cctcg agagg	ctcca tcgga	acctc 1260	
cttaag	cgc tgcag	gggg gaaga	agctc ctttg	gctct accac	gaggt ggaaa	agccc 1320	
ctctccc	ggg tccct	ggccc tatgg	aggcc accgg	gggtac ggcgg	gacgt ggcct	acctt 1380	
caggccc	cttt ccttg	agct tgcgg	aggag atccg	cgc tgcag	gagga ggtct	tccgc 1440	
ttggc	gggg acccc	cttca cctca	actcc cggga	cacc tggaa	aggg gctct	tttgac 1500	
gagctt	aggc ttccc	agttt gaaga	agacg aaga	agacg gcaag	cgcctc caccag	cgc 1560	
gcggtg	ctgg aggcc	ctacg ggagg	ccac cccat	cgtgg agaag	atcct ccagc	accgg 1620	
gagctc	acca agct	caaga cacct	acgtg gaccc	cctcc caagc	ctcgt ccaccc	gagg 1680	
acggg	ccgc tccac	acccg ctcca	accag acggc	cacgg ccacg	gggag gctta	gtagc 1740	
tccga	cccc acct	gcaga catccc	cgtc cgcac	ccct tgggc	cagag gatcc	gccgg 1800	
gccttc	gtgg ccgag	gggg ttggg	cgttg gtggc	ccttg actat	agcca gatag	agctc 1860	
cgcgtc	ctcg cccac	ctct cgggg	acgaa aacct	gatca gggct	ctcca ggagg	ggaag 1920	
gacatc	caca cccag	accgc aagct	ggatg ttcgg	cgtcc ccccg	aggc cgtgg	acccc 1980	
ctgatg	cgc gggcg	ccaa gacgg	tgaac ttcgg	cgtcc totac	ggcat gtccg	cccat 2040	
aggctc	ctcc aggag	cttgc catccc	ctac gaggag	gcgg tggc	ctttat agagc	gctac 2100	
ttccaa	agct tcccc	aaggt gcggg	ccttg atag	aaaaga ccctg	gagga gggg	aggaag 2160	
cgggg	ctac tggaa	accct cttcg	gaaga aggcg	ctac tgccc	gacct caacg	cccgg 2220	
gtgaag	agcg tcagg	gaggc cgcgg	agcgc atgg	ccttc acatg	cccgt ccagg	gcacc 2280	
gccgcg	accc tcatg	aagct cgcct	atg cccgc	ctccg ggagat	gggg 2340		
gcccgc	atgc tctcc	aggt cgcca	acgag ctctc	cttg agggc	cccca agcgc	ggggc 2400	
gaggag	gtgg cggct	tttgg caagg	aggcc atgg	agaagg cctat	cccct cgccg	tgcc 2460	
ctggag	gtgg aggtg	gggg gat	ggggagg	ac tggct	tttccg ccaagg	t 2508	

<210> 418

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 418

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
245 250 255
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
260 265 270
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
290 295 300
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305 310 315 320
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
325 330 335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
340 345 350
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
355 360 365
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
370 375 380
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385 390 395 400
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
405 410 415
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
420 425 430
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
435 440 445
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
450 455 460
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465 470 475 480
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
485 490 495
Val Leu Phe Asp Glu Leu Arg Leu Pro Ser Leu Lys Lys Thr Lys Lys
500 505 510
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
515 520 525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
530 535 540
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545 550 555 560
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
565 570 575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
580 585 590
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
595 600 605
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 419

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 419

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaagccc cctccttcg ccacgaggcc	240

tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgagggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcggtggg gacccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttctt ggagaggctg	840
gagttcgga gcctcctcca cgagttcggc ctcttgagg cccccgccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tctctctccg ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca	1020
gacccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctcgtgccc gggacgacct catgctctc	1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcgcg ctacgggggg	1200
gagtggacgg aggacgcgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc	1320
ctctcccggg tcttgggcca tatggaggcc accggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccctggagct tgcggaggag atccgcgcgc tcgaggagga ggtcttccgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac	1500
gagcttaggc ttccgcctt gaagaagacg aagaagacag gcaagcgctc caccggtgcc	1560
gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg	1680
acgggcccgc tccacaccgc cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgacccca acctgcagaa catccccgtc cgcacccct tgggcccagag gatccgcgg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgctctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag	1920
gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgaggc cgtggacccc	1980
ctgatgcgc gggcgccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac	2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100

ttccaaagct tccccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
 cggggctacg tggaaccct cttcggaaga aggcgctacg tgcccacac caacgcccgg 2220
 gtgaagagcg tcagggaggg cgcgagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgcccacc tcatgaagct cgccatgggt aagctcttcc cccgcctccg ggagatgggg 2340
 gcccgcatgc tctccaggt cgccaacgag ctctcctgg agggccccc agcgcgggcc 2400
 gaggaggtgg cggtttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt 2508

<210> 420

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 420

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Gly Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 421
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> n
 <222> (16)..(18)
 <223> n is any base a,t,c, or g.
 <400> 421
 ggcaagcgct ccaccnnngc cgcggtgctg gagggccctac gg 42
 <210> 422
 <211> 15
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 422
 ggtggagcgc ttgcc 15
 <210> 423
 <211> 2508
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 423
 atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
 ggggtacaagg cgtcttcgt ggtctttgac gccaaagggc cctccttcgc ccacgaggcc 240
 tacgaggcct acaaggcggg gagggcccg acccccgagg acttcccccg gcagctcgcc 300
 ctcacaaagg agctggtgga cctcctgggg ttaccgcc tcgaggtccc cggctacgag 360

gcggacgacg	ttctcgccac	cctggccaag	aaggcgga	aggaggggta	cgaggtgcgc	420
atcctcaccg	ccgaccgga	cctctacaa	ctcgtctccg	accgctgcgc	cgctctccac	480
cccagggggc	acctcatcac	cccggagtgg	ctttgggaga	agtacggcct	caggccggag	540
cagtgggtgg	acttccgcgc	cctcgtgggg	gacccctccg	acaacctccc	cggggtcaag	600
ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggcccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cggtgcgcga	ccgacctccc	cctggaggtg	780
gacctcgccc	aggggcggga	gcccgaccgg	gaggggctta	gggccttcct	ggagaggctg	840
gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	ccccgcctcc	cctggaggag	900
gccccctggc	ccccgcggga	aggggccttc	gtgggcttcg	tcctctcccg	ccccgagccc	960
atgtgggcgg	agcttaaagc	cctggccgcc	tgcaggggcg	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccagggggg	tggcgcggcg	ctacgggggg	1200
gagtggacgg	aggacgccgc	ccaccgggcc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctcccggg	tcctggccca	tatggaggcc	accgggggtac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcggggc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggg	gctctttgac	1500
gagcttaggc	ttcccgctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagctta	1560
gcggtgctgg	aggccctacg	ggaggccac	cccatcgtgg	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccctcc	caagcctcgt	ccacccgagg	1680
acgggccgcc	tcacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tcgacccca	acctgcagaa	catccccgtc	cgcacccct	tgggcccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtctcgc	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catccccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	tcccaaggt	gcgggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaacct	cttcggaaga	aggcgctacg	tgcccacct	caacgcccgg	2220

gtgaagagcg tcagggagggc cgcgagagcg atggccttca acatgcccgt ccagggcacc 2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcatgc tctccaggt cgccaacgag ctctctctgg agggccccca agcgcgggcc 2400
gaggaggtgg cggttttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt 2508

<210> 424

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 424

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Leu Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 425
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> n
 <222> (19) .. (21)
 <223> n is any base a,t,c, or g.
 <400> 425
 ggcaagcgct ccaccagcnn ngcgggtgctg gagggcctac gg 42
 <210> 426
 <211> 2508
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 426
 atgaattcgc aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctgggtggac 60
 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
 ggggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgc ccacgaggcc 240
 tacgaggcct acaaggcggg gagggccccg acccccagagg acttcccccg gcagctcgcc 300
 ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag 360
 gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
 atcctcaccg ccgaccgcga cctctaccaa ctctgtctcg accgcgtcgc cgtcctccac 480
 cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
 cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cgggggtcaag 600
 ggcacgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
 ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggccacctg 720
 gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780

gacctcgccc aggggcgggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tctctcccc ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca	1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgaccc catgtctctc	1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcgggc ctacgggggg	1200
gagtggacyg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc ctttggtct accacgaggt ggaaaagccc	1320
ctctccccgg tcttggccca tatggaggcc accggggtac ggcgggacgt ggacctactt	1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttcgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac	1500
gagcttaggc ttcccgctt gaagaagacg aagaagacag gcaagcgctc caccagccgt	1560
gcggtgctgg aggcctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctcacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg	1680
acgggcgcgc tccacaccgc cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgaccca acctgcagaa catccccgtc cgcacccctc tgggcccagag gatccgccgg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag	1920
gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgaggc cgtggacccc	1980
ctgatgcgcc gggcgggcaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac	2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100
ttccaaagct tccccaaggt gcgggccttg atagaaaaga ccctggagga ggggaggaag	2160
cggggctacg tggaaacctt cttcggaaga aggcgtacg tgcccaccc caacgcccgg	2220
gtgaagagcg tcaggaggc cgcgagcgc atggccttca acatgcccgt ccagggcacc	2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg	2340
gcccgcacgc tctccaggt cgccaacgag ctctctctgg agggccccca agcgcggggc	2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc	2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt	2508

<210> 427

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 427

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Arg Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 428

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 428

atgaattcgg	ggatgctgcc	cctctttgag	cccaagggcc	gggtcctcct	ggtggacggc	60
caccacctgg	cctaccgcac	cttcacgcc	ctgaagggcc	tcaccaccag	ccggggggag	120
ccggtgcagg	cgggtctacg	cttcgccaag	agcctcctca	aggccctcaa	ggaggacggg	180
gacgcggtga	tcgtggtctt	tgacgccaag	gccccctcct	tccgccacga	ggcctacggg	240
gggtacaagg	cgggccgggc	ccccacggcg	gaggactttc	cccggcaact	cgccctcatc	300
aaggagctgg	tggacctcct	ggggctggcg	cgctctgagg	tcccgggcta	cgaggcggac	360
gacgtcctgg	ccagcctggc	caagaaggcg	gaaaaggagg	gctacgaggt	ccgcatcctc	420
accgccgaca	aagaccttta	ccagctcctt	tccgaccgca	tccacgtcct	ccaccccag	480
gggtacctca	tcaccccggc	ctggctttgg	gaaaagtagc	gcctgaggcc	cgaccagtgg	540
gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccggggg	caagggcatc	600
ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
aagctctcct	gggacctggc	caaggtgcgc	accgacctgc	ccctggaggt	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggccccctgg	900
cccccgccgg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtggggc	960
gatctttctg	ccctggccgc	cgccaggggc	ggccgcgtcc	accgggcccc	cgagccttat	1020
aaagccctca	gggacctgaa	ggaggcgccg	gggcttctcg	ccaaagacct	gagcgttctg	1080
gccctgaggg	aaggccttgg	cctcccgcgc	ggcgacgacc	ccatgctcct	cgcctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcccggc	gctacggcgg	ggagtggacg	1200
gaggaggcgg	gggagcgggc	cgccctttcc	gagaggctct	tcgccaacct	gcttaagagg	1260
cttgaggggg	aggagaggct	ccttttgctt	taccgggagg	tggagaggcc	cctttccgct	1320
gtcctggccc	atatggaggc	cacgggggtg	cgccgggacg	tggcctatct	cagggccttg	1380
tccctggagg	tggccgagga	gatcgccgc	ctcgaggccg	aggtcttccg	cctggccggc	1440
cacccttca	acctcaactc	ccgggaccag	ctggaaaggg	tcctctttga	cgagctaggg	1500
cttcccgcga	tcaagaagac	gcaaaagacc	ggcaagcgct	ccaccagcgc	cgccgtcctg	1560
gaggccctcc	gcgaggccca	ccccatcgtg	gagaagatcc	tgcagtaccg	ggagctcacc	1620
aagctgaaga	gcacctacat	tgacctcttg	ccggacctca	tccaccccag	gacgggccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggca	ggctaagtag	ctccgatccc	1740
aacctccaga	acatccccgt	ccgcaccccg	cttgggcaga	ggatccgccc	ggccttcac	1800
gccgaggagg	ggtggctatt	ggtggccctg	gactatagcc	agatagagct	caggggtgctg	1860

gccacacct cccgacga gaacctgac cgggtcttcc aggagggcg ggacatccac 1920
 acggagaccg ccagctggat gttcggcgtc ccccgggagg ccgtggaccc cctgatgcgc 1980
 cgggaggcca agaccatcaa cttcgggggtc ctctacggca tgcgggcca ccgcctctcc 2040
 caggagctag ccatccctta cgaggaggcc caggccttca ttgagcgcta ctttcagagc 2100
 ttccccaagg tgcgggctg gattgagaag accctggagg agggcaggag gcgggggtac 2160
 gtggagaccc tcttcggccg ccgccgtac gtgccagacc tagaggcccg ggtgaagagc 2220
 gtgcgggagg cggccgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcataagc tggctatggt gaagctcttc ccaggctgg aggaaatggg ggccaggatg 2340
 ctccttcagg tcgccaacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400
 gcccggtgg ccaaggaggt catggagggg gtgtatcccc tggcgtgcc cctggaggtg 2460
 gaggtgggga taggggagga ctggctctcc gccaaaggag 2499

<210> 429

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 429

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1			5						10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65				70					75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85					90						95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				

Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	225	230	235	240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	245	250	255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	260	265	270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	275	280	285	
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	290	295	300	
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	305	310	315	320
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	325	330	335	
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	340	345	350	
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	355	360	365	
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	370	375	380	
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	385	390	395	400
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	405	410	415	
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	420	425	430	
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	435	440	445	
Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	450	455	460	
Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	465	470	475	480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Gln Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu

<210> 430

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 430

acgggggtgc gccgggacgt ggcctat

27

<210> 431

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 431

atgaattccg aggcgatgct tccgctcttt gaaccctaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccgggtgc aggcgggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg cgtcttcgt ggtctttgac gccaaaggccc cctccttcgg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccc acccccagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctaccaa ctctgtctcc accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac ccgggagtg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggtg	780

gacctcgccc aggggcgggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcgga gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc	960
atgtgggagg agcttaaagc cctggccgcc tgcaggggag gccgcgtgca ccgggcagca	1020
gacctcttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctctgtcccg gggacgaccc catgctcctc	1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcgagg ctacgggggg	1200
gagtggacgg aggacggcg ccaccgggccc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc ctttggtct accacgaggt ggaaaagccc	1320
ctctcccggg tcctggccca tatggaggcc accgggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccttgaggct tgcggaggag atccgcccgc tcgaggagga ggtcttcgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac	1500
gagcttaggc ttcccaagtt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggcctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg	1680
acgggcccgc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgacccca acctgcagaa catccccgtc cgcacccct tgggcccagag gatccgcccg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag	1920
gacatccaca cccagaccgc aagctggatg ttccggctcc ccccgaggc cgtggacccc	1980
ctgatgcgc gggcgcccaa gacggtgaac ttccggctcc tctacggcat gtccgcccac	2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100
ttccaaagct tcccaaggt gcgggcctgg atagaaaaga ccttgaggga ggggaggaag	2160
cggggctacg tggaaacct cttcggaaga aggcgtacg tgcccgacct caacgcccgg	2220
gtgaagagcg tcaggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc	2280
gccgcccacc tcatgaagct cgcctggtg aagctcttcc cccgcctccg ggagatgggg	2340
gcccgcacgc tcctccaggt cgccaacgag ctctcctcgg agggccccca agcgcggggc	2400
gaggaggtgg cggttttggc caaggaggcc atggagaagg cctatccct cgcggtgccc	2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt	2508

<210> 432

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 432

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Lys Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 433

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 433	
cttaggcttc ccaagttgaa gaagacgaag aagaca	36
<210> 434	
<211> 36	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 434	
tgtcttcttc gtcttcttca acttggaag cctaag	36
<210> 435	
<211> 2508	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 435	
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg cactttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaagccc cctccttcgg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctaccaa ctctgtctcg accgctcgcc cgtcctccac	480
cccgagggcc acctcatcac ccgggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctctggagg cccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc	960

atgtgggagg	agcttaaagc	cctggccgcc	tgcaggggag	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccagggggg	tggcgcgggc	ctacgggggg	1200
gagtggacgg	aggacgccc	ccaccggg	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctccccgg	tcctggccca	tatggaggcc	accgggggtac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcgggcc	acccttcaa	cctcaactcc	cgggaccagc	tggaaagggg	gctctttgac	1500
gagcttaggc	ttcccgctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	agggccctacg	ggaggccac	cccatcgtgg	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccctcc	caagcctcgt	ccaccgagg	1680
acgggcccgc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tcgacccca	acctgcagaa	catccccgtc	cgcacccct	tgggccagag	gatccgcccg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatcgcca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	ttcccaaggt	gcgggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgcccacact	caacgcccgg	2220
gtgaagagcg	tcaggagggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgccgacc	tcatgaagct	cgccatggtg	aagctcttcc	ccgcctccg	ggagatgggg	2340
gcccgcacgc	tcctccaggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcggggc	2400
gaggaggtgg	cggttttggc	caaggaggcc	atggagaagg	cctatccctc	cgcctgccc	2460
ctggaggtgg	aggtggggat	gggggaggac	tggctttccg	ccaagggt		2508
<210> 436						
<211> 836						
<212> PRT						

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 436

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15
Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
245 250 255
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
260 265 270
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
290 295 300
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305 310 315 320
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
325 330 335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
340 345 350
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
355 360 365
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
370 375 380
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
385 390 395 400
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
405 410 415
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
420 425 430
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
435 440 445
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
450 455 460
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465 470 475 480
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
485 490 495
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
500 505 510
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
515 520 525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
530 535 540
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545 550 555 560
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
565 570 575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
580 585 590
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
595 600 605
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile Ala Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 437

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 437

gaggggaagg acatcgccac ccagaccgca agc

33

<210> 438

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 438

gcttgcggtc tgggtggcga tgccttccc etc

33

<210> 439

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 439

atgaattccg aggcgatgct tccgtctttt gaacccaaag gccgggtcct cctggtggac 60

ggccaccacc tggcctaccg caccttcttc gccctgaagg gctcaccac gagccggggc 120

gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180

gggtacaagg cgtcttcgt ggtctttgac gccaaggccc cctccttcgg ccacgaggcc 240

tacgaggcct acaaggcggg gagggccccg acccccagagg acttcccccg gcagctcgcc 300

ctcatcaagg agctggtgga cctcctgggg tttaccgccg tcgagggtccc cggctacgag 360

gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgagggtgcg 420

atcctcaccg ccgaccgcca cctctaccaa ctctgtctcg accggtctgc cgtcctccac 480

cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540

cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cgggggtcaag 600

ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660

ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720

gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780

gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttctt ggagaggctg 840

gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag 900

gccccctggc ccccgccgga aggggccttc gtgggcttcg tctctctccg ccccgagccc 960

atgtgggcgg agcttaaagc cctggccgcc tgcagggggc gccgcgtgca ccgggcagca 1020

gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccgaggggg	tggcgcgggc	ctacgggggg	1200
gagtggacgg	aggacgccc	ccaccggggc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctccccgg	tcctggccca	tatggaggcc	accgggggtac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcgaggagg	atccgcccgc	tcgaggagga	ggtcttccgc	1440
ttggcgggcc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttcccgccct	gaagaagccg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgctg	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccctccc	caagcctcgt	ccacccgagg	1680
acggggccgc	tccacacccg	cttcaaccag	acggccacgg	ccacgggggag	gcttagtagc	1740
tccgacccca	acctgcagaa	catccccgtc	cgcaccccct	tgggccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgtcc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgtcc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	tccccaaagg	gcgggccttg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgccccacct	caacgcccgg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgccgacc	tcatgaagct	cgccatggtg	aagctcttcc	cccgccctccg	ggagatgggg	2340
gcccgcacgc	tcctccaggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcggggc	2400
gaggaggtgg	cggcttttgg	caaggaggcc	atggagaagg	cctatcccct	cgcctgtccc	2460
ctggaggtgg	aggtggggat	gggggaggac	tggctttccg	ccaagggt		2508

<210> 440

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 440

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	210	215	220	
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	225	230	235	240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	245	250	255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	260	265	270	
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	275	280	285	
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300	
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	305	310	315	320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Pro Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

<400> 442
cttgctgtc ttcttcggct tcttcaaggc ggg

33

<210> 443

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 443

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc	60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccggggggag	120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggcctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggcccggc cccacgcgcg gaggactttc cccggcaact cgcctcatc	300
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag	480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg	720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc	780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc	840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg	900
ccccgcggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc	960
gatcttctgg ccctggccgc cgccaggggc ggccgcgttt accgggcgga ggatcccttg	1020
gaggccttgc gggggcttgg ggaggtgagg gggcttttgg ccaaggacct ggcggtgctg	1080
gcctgaggga aagggattgc cctggcaccg ggcgacgacc ccatgctcct cgcctacctc	1140
ctggatcctt ccaacaccgc cccgaaggg gtagcccggc gctacggggg ggagtggacc	1200
gaggaggcgg gggaaagggc gctgctttcc gaaaggcttt acgccgccct cctgaagcgg	1260
cttaaggggg aggagaggct tctttggctt tacgaggagg tggaaaagcc cctttcgcgg	1320
gtcctggccc acatggaggc cacgggggta cggttggatg tggcctactt aaaggccctt	1380

tccctggagg	tggaggcgga	gataaggcgc	ttcgaggagg	aggtccaccg	cctggccggg	1440
catcctttca	acctgaactc	ccgggaccag	ctggaaaggg	tcatctttga	cgagcttggg	1500
cttcccgcca	tcaagaagac	gaggaagacg	ggcaagcgct	ccaccagcgc	cgccgttttg	1560
gaggccttgc	gggagggtca	tcccatcgtg	gaccgcatcc	ttcagtaccg	ggagctttcc	1620
aagctcaagg	gaacctacat	cgatcccttg	cctgcccttg	tccaccccaa	gacgaaccgc	1680
ctccacaccc	gtttcaacca	gacggccacc	gccacgggga	ggcttagcag	ctcggatcct	1740
aatctgcaaa	atatccccgt	gcgcacccct	ttgggccagc	ggatccgccg	ggccttcgtg	1800
gccgaggagg	ggtggaggct	ggtggttttg	gactacagcc	agattgagct	cagggtcctg	1860
gcgcaccttt	ccggggacga	gaacctaatc	cgggtcttcc	aggagggcca	ggacatccac	1920
accagacgg	ccagctggat	gttcggcgtg	ccccagagg	ccgtggattc	cctgatgcgc	1980
cgggcgggcca	agaccatcaa	cttcggcgtc	ctctacggca	tgtccgcccc	ccggctttcg	2040
ggagagctgg	ccatccccta	cgaggaggcg	gtggccttca	tcgagcggtg	tttccagagc	2100
tacccaagg	tgcgggcctg	gattgagaaa	accctggcgg	aaggacggga	acggggctat	2160
gtggaaaccc	tctttggccg	ccggcgctac	gtgcccgact	tggcttcccg	ggtgaagagc	2220
atccgggagg	cagcggagcg	catggccttc	aacatgccgg	tccaggggac	cgccgcggat	2280
ttgatgaaac	tggccatggt	gaagctcttt	cccaggcttc	aggagctggg	ggccaggatg	2340
cttttgacagg	tgcacaacga	actggtcctc	gaggctccca	aggagcaagc	ggaggaagtc	2400
gcccaggagg	ccaagcggac	catggaggag	gtgtggcccc	tgaagggtgcc	cttggagggtg	2460
gaagtgggca	tcggggagga	ctggctttcc	gccaaaggcc			2499

<210> 444

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 444

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	

Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		

Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val Tyr Arg Ala
 325 330 335
 Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu
 355 360 365
 Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala
 405 410 415
 Leu Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val
 450 455 460
 Glu Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val
 595 600 605
 Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser
725 730 735
Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765
Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val
770 775 780
His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val
785 790 795 800
Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val
805 810 815
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Ala

<210> 445

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 445

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctcctct ggtggacggc 60
caccacctgg cctaccgcac ctccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cgggtctacgg ctccgccaaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggccctacggg 240
gggtacaagg cgggcccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780

aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc	840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg	900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc	960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtcc accgggcaac aagccccggtt	1020
gaggccctgg ccgacctcaa ggaggccccg gggttcctgg ccaaggacct ggccgttttg	1080
gccctgcggg aggggggtggc cctggacccc acggacgacc ccctcctggt ggccctacctc	1140
ctggacccgg ccaacaccca cccgagggg gtggcccggc gctacggggg cgagttcacg	1200
gaggacgcag cggagagggc cctcctctcc gagaggctct tccagaacct ctttaaacgg	1260
ctttccgaga agctcctctg gctctaccag gaggtggagc ggccccctct ccgggtcttg	1320
gcccatatgg agggccgggg ggtgaggctg gacgtccccc ttctggaggc cctctccttt	1380
gagctggaga aggagatgga gcgcctggag ggggaggtct tccgtttggc cgcccacccc	1440
ttcaacctca actccgcga ccagctggaa agggtcctct ttgacgagct gggcctcacc	1500
ccggtgaagc ggacgaagaa gacgggcaag cgctccaccg cccagggggc cctggaggcc	1560
ctccgggggg cccaccccat cgtggagctc atcctccagt accgggagct ttccaagctc	1620
aaaagcacct acctggaccc cctgccccgg ctcgccacc cgccggacggg ccggctccac	1680
accgccttca accagacggc cacggccacg ggaaggcttt ccagctccga ccccaacctg	1740
cagaacatcc ccgtgcgcac ccccttgggg cagcgcaccc gcaaggcctt cgtggccgag	1800
gaggggtggc tccttttggc ggcggactac tcccagattg agctccgggt cctggccccac	1860
ctctcggggg acgagaacct gaagcgggtc ttccgggagg ggaaggacat ccataccgag	1920
accgccgcct ggatgttcgg cttagacccc gctctggtgg atccaaagat gcgccgggcg	1980
gccaagacgg tcaacttcgg cgtcctctac gggatgtccg cccacaggct ctcccaggag	2040
ctcggcatag actacaagga ggcggaggcc ttatttgagc gctacttcca gagcttcccc	2100
aaggtgcggg cctggataga aaggaccctg gaggagggcc ggacgcgggg ctacgtggag	2160
accctgttcg gcaggaggcg ctatgtgccc gacctggcct cccgggtccg ctccgtgcgg	2220
gaggcggcgg agcggatggc cttcaacatg cccgtgcagg gcaccgcccgc cgacctgatg	2280
aagatcgcca tggatcaagct cttccccagg ctaaagcccc tgggggcccc cctcctctc	2340
caagtggcca acgagctggt cctggagggtg cccgaggacc gggccgagga ggccaaggcc	2400
ctggatcaagg aggtcatgga gaacgcctac cccctggacg tgccccctga ggtggagggtg	2460
ggcgtgggtc gggactggct ggaggcgaag caggat	2496

<210> 446

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 446

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305 310 315 320
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
325 330 335
Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala Arg Gly Phe
340 345 350
Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Val Ala Leu
355 360 365
Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu Asp Pro Ala
370 375 380
Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Phe Thr
385 390 395 400
Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Gln Asn
405 410 415
Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr Gln Glu Val
420 425 430
Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Arg Gly Val
435 440 445
Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu Leu Glu Lys
450 455 460
Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala Gly His Pro
465 470 475 480
Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
485 490 495
Leu Gly Leu Thr Pro Val Lys Arg Thr Lys Lys Thr Gly Lys Arg Ser
500 505 510
Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His Pro Ile Val
515 520 525
Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Ser Thr Tyr
530 535 540
Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly Arg Leu His
545 550 555 560
Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
565 570 575
Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
580 585 590

Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu Leu Ala Ala
 595 600 605
 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
 610 615 620
 Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile His Thr Glu
 625 630 635 640
 Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val Asp Pro Lys
 645 650 655
 Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met
 660 665 670
 Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr Lys Glu Ala
 675 680 685
 Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala
 690 695 700
 Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly Tyr Val Glu
 705 710 715 720
 Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg Val
 725 730 735
 Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
 740 745 750
 Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val Lys Leu Phe
 755 760 765
 Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln Val Ala Asn
 770 775 780
 Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu Ala Lys Ala
 785 790 795 800
 Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp Val Pro Leu
 805 810 815
 Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala Lys Gln Asp
 820 825 830

<210> 447

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 447

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg cegtcttcgt ggtctttgac gccaaagccc cctccttccg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgccg tcgaggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctaccaa ctctctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttctt ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctcttgagg cccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tctctccccg ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggag gccgcgttta ccgggcggag	1020
gatcccttgg aggccttgcg ggggcttggg gaggtgaggg ggcttttggc caaggacctg	1080
gcggtgctgg ccctgaggga agggattgcc ctggcaccgg gcgacgacct catgctctc	1140
gcctacctcc tggatccttc caacaccgcc cccgaagggg tagcccggcg ctacgggggg	1200
gagtggaccg aggaggcggg ggaaaggcg ctgctttccg aaaggcttta cgccgcctc	1260
ctgaagcggc ttaaggggga ggagaggctt ctttggcttt acgaggagggt ggaaaagccc	1320
ctttcgcggg tcttgcccca catggaggcc acgggggtac gggttgatgt ggcctactta	1380
aaggcccttt ccctggagggt ggaggcggag ataaggcgt tcgaggagga ggtccaccgc	1440
ctggccgggc atcctttcaa cctgaactcc cgggaccagc tggaaagggt catctttgac	1500
gagcttgggc ttcccgccat caagaagacg aggaagacgg gcaagcgctc caccagcgcc	1560
gccgttttgg aggccttgcg ggaggctcat cccatcgtgg accgcatcct tcagtaccgg	1620
gagctttcca agctcaaggg aacctacatc gatcccttgc ctgccctggg ccaccccaag	1680
acgaaccgcc tccacaccg tttcaaccag acggccaccg ccacggggag gcttagcagc	1740
tcggatccta atctgcaaaa tatccccgtg cgcacccctt tgggcccagc gatccgcccg	1800
gccttcgtgg ccgaggagggt gtggaggctg gtggttttgg actacagcca gattgagctc	1860

agggtcctgg cgcacctttc cggggacgag aacctaatacc gggctctcca ggagggccag 1920
 gacatccaca cccagacggc cagctggatg ttcggcgtgc cccagaggc cgtggattcc 1980
 ctgatgcgcc gggcgccaa gaccatcaac ttcggcgtcc tctacggcat gtccgcccac 2040
 cggctttcgg gagagctggc catccctac gaggaggcgg tggccttcat cgagcggat 2100
 ttccagagct accccaaggt gcgggcctgg attgagaaaa ccctggcgga aggacgggaa 2160
 cggggctatg tggaaaccct ctttggccgc cggcgctacg tgcccgaact ggcttcccgg 2220
 gtgaagagca tccgggaggc agcggagcgc atggccttca acatgccggg ccaggggacc 2280
 gccgcggatt tgatgaaact ggccatggtg aagctctttc ccaggcttca ggagctgggg 2340
 gccaggatgc ttttgcaggt gcacaacgaa ctggtcctcg aggctcccaa ggagcaagcg 2400
 gaggaagtcg cccaggaggc caagcggacc atggaggagg tgtggcccct gaaggtgccc 2460
 ttggagggtg aagtgggcat cggggaggac tggctttccg ccaaggcc 2508

<210> 448

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 448

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
			85						90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
		100						105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 Tyr Arg Ala Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly
 355 360 365
 Ile Ala Leu Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 Tyr Ala Ala Leu Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp
 420 425 430
 Leu Tyr Glu Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser
 450 455 460

Leu Glu Val Glu Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Ile Phe Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys
 530 535 540
 Leu Lys Gly Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys
 545 550 555 560
 Thr Asn Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp
 595 600 605
 Arg Leu Val Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Ala Ser Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala
 785 790 795 800

Glu Glu Val Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro
 805 810 815
 Leu Lys Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Ala
 835

<210> 449

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 449

```

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac      60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc      120
gaaccgggtgc aggcgggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac      180
gggtacaagg ccgctcttcgt ggtctttgac gccaaggccc cctccttcog ccacgaggcc      240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc      300
ctcatcaagg agctggtgga cctcctgggg tttaccogcc tcgaggctcc cggctacgag      360
gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc      420
atcctcaccg ccgaccgga cctctaccaa ctcgctcctc accgcgtcgc cgtcctccac      480
cccgaggggc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag      540
cagtgggttg acttcgcgc cctcgtgggg gaccctcctc acaacctccc cgggggtcaag      600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc      660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg      720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg      780
gacctcgccc aggggcgggg gcccgaccgg gaggggctta gggccttctt ggagaggctg      840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag      900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc      960
atgtgggcgg agcttaaagc cctggccgcc tgcagggggc gccgcgtcca ccgggcaaca     1020
agcccggttg aggccttggc cgacctcaag gagggccggg ggttcctggc caaggacctg     1080
gccgttttgg ccctgcggga gggggtggcc ctggaccca cggacgaccc cctcctggtg     1140
gcctacctcc tggaccgggc caacaccac cccgaggggg tggcccgggc ctacgggggc     1200
  
```

gagttcacgg aggacgcagc ggagaggggcc ctctctccg agaggctctt ccagaacctc	1260
tttaaacggc tttccgagaa gctcctctgg ctctaccagg aggtggagcg gccctctcc	1320
cgggtcttgg cccacatgga ggcccggggg gtgaggctgg acgtccccct tctggaggcc	1380
ctctcctttg agctggagaa ggagatggag cgcctggagg gggaggctctt ccgtttggcc	1440
ggccaccctt tcaacctcaa ctcccgcgac cagctggaaa gggtcctctt tgacgagctg	1500
ggcctcacc cggatgaagcg gacgaagaag acgggcaagc gctccaccgc ccagggggcc	1560
ctggaggccc tccggggggc ccaccccatc gtggagctca tcctccagta ccgggagctt	1620
tccaagctca aaagcaccta cctggacccc ctgccccggc tcgtccacc gcggacgggc	1680
cggctccaca cccgcttcaa ccagacggcc acggccacgg gaaggctttc cagctccgac	1740
cccaacctgc agaacatccc cgtgcgcacc cccttggggc agcgcacccg caaggccttc	1800
gtggccgagg aggggtggct ccttttggcg gcggactact ccagattga gctccgggtc	1860
ctggcccacc tctcggggga cgagaacctg aagcgggtct tccgggaggg gaaggacatc	1920
cataccgaga ccgccgcctg gatgttcggc ttagaccccg ctctggtgga tccaaagatg	1980
cgccgggcgg ccaagacggt caacttcggc gtctctacg ggatgtccgc ccacaggctc	2040
tcccaggagc tcggcataga ctacaaggag gcggaggcct ttattgagcg ctacttccag	2100
agcttcccca aggtgcgggc ctggatagaa aggaccctgg aggagggccg gacgcggggc	2160
tacgtggaga ccctgttcgg caggaggcgc tatgtgccg acctggcctc ccgggtccgc	2220
tcggtgcggg agggcgcgga gcggatggcc ttcaacatgc ccgtgcaggg caccgccgc	2280
gacctgatga agatcgccat ggtcaagctc ttccccaggc taaagcccct gggggcccac	2340
ctctcctcc aagtggccaa cgagctggtc ctggaggctc ccgaggaccg ggccgaggag	2400
gccaaaggccc tggatcaagga ggtcatggag aacgcctacc cctggacgt gccctcgag	2460
gtggagggtg gcgtgggtcg ggactggctg gaggcgaagc aggat	2505

<210> 450

<211> 835

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 450

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	210	215	220	
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	225	230	235	240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	245	250	255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	260	265	270	
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	275	280	285	
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300	
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	305	310	315	320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala
 340 345 350
 Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly
 355 360 365
 Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 Phe Gln Asn Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu
 450 455 460
 Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Gly Leu Thr Pro Val Lys Arg Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His
 515 520 525
 Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys
 530 535 540
 Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu
 595 600 605
 Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val
 645 650 655

Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr
 675 680 685
 Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala
 725 730 735
 Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln
 770 775 780
 Val Ala Asn Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu
 785 790 795 800
 Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala
 820 825 830

Lys Gln Asp
835

<210> 451

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 451
 cttctctcat cgcgcaaaac agcc

24

<210> 452

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 452

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcc tcgaggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctaccaa ctctctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctcttgagg cccccgccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tctctcccc ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca	1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgacct catgctctc	1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcgcg ctacgggggg	1200
gagtggaagg aggacgcgc ccaccgggc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc	1320
ctctcccggg tcttggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccttgagct tgcggaggag atccgccgcc tcgaggagga ggtcttcgc	1440
ttggcggggc accccttcaa cctcaactcc cgggaccagc tggaaaggg gctctttgac	1500
gagcttaggc ttccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggcctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccaccgagg	1680
acgggcgcgc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgaccca acctgcagaa catccccgtc cgcacccctc tgggccagag gatccgccg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860

cgcgctcctcg cccacctctc cggggacgaa aacctgatca gggctcttcca ggaggggaag 1920
 gacatccaca ccagaccgc aagctggatg ttcggcgctcc ccccgaggc cgtggacccc 1980
 ctgatgcgcc gggcggccaa gacggtgaac ttcggcgctcc tctacggcat gtccgcccac 2040
 aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
 ttccaaagct tcccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
 cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgcacct caacgcccgg 2220
 gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gcccgcatgc tcctccaggt cgccaacgag ctctctctgg agggccccca agcgcgggcc 2400
 gaggaggtgg cggttttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaaggggtca ccaccaccac 2520
 caccac 2526

<210> 453

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 453

ctctccacg agttcggc

18

<210> 454

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 454

atgaattccc tgccctctt tgagcccaag ggccgggtgc ttctggtgga cgccaccac

60

ctggcctacc gtacctttt tgccctgaag ggcctcacca ccagccgagg ggagccggtc

120

caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg

180

gtgatcgtgg tgtttgacgc caaggcccc tccttcgcc accagacctg cgaggcctac

240

aaggcggggc gggctcccac ccccgaggac tttccccggc agcttgccct tatcaaggag

300

atggtggacc	ttttgggctt	tacccgcctc	gaggtgccgg	gctttgaagc	ggatgacgtc	360
ctggctaccc	tggccaagaa	ggcggaaaag	gaaggctacg	aagtgcgcac	cctcaccgcg	420
gaccgggacc	tttaccagct	tctttcggag	cgaatctcca	tccttcaccc	ggaggggttac	480
ctgatcacc	cggagtggct	ttgggagaag	tatgggctta	agccttccca	gtgggtggac	540
taccgggcct	tggccgggga	cccttcgcac	aacatccccg	gcgtgaaggg	catcggggag	600
aagacggcgg	ccaagctgat	ccgggagtgg	ggaagcctgg	aaaaccttct	taagcacctg	660
gaacaggtga	aacctgcctc	cgtgcggggag	aagatcctta	gccacatgga	ggacctcaag	720
ctatccctgg	agctatcccc	ggtgcacacg	gacttgctcc	ttcaggtgga	cttcgccccg	780
cgccgggagc	cggaccggga	ggggcttaag	gccttttttg	agaggctgga	gttcggaagc	840
ctcctccacg	agttcggcct	gttggaaagc	ccggtggcgg	cggaggaagc	tccttggccg	900
cccccgagg	gagccttcgt	ggggtacgtt	ctttcccgcc	ccgagcccat	gtgggcggag	960
cttaacgcct	tggccgccgc	ctggggcggc	cgcgtgcacc	gggcagcaga	ccccttggcg	1020
gggctaaagg	acctcaagga	ggtccggggc	ctcctcgcca	aggacctcgc	cgtcttggcc	1080
tcgagggagg	ggctagacct	cgtgcccggg	gacgacccca	tgctcctcgc	ctacctctg	1140
gaccttcga	acaccacccc	cgaggggggtg	gcgcggcgct	acggggggga	gtggacggag	1200
gacgcgccc	accgggccct	cctctcggag	aggctccatc	ggaacctcct	taagcgcctc	1260
gagggggagg	agaagctcct	ttggctctac	cacgaggtgg	aaaagcccct	ctcccgggtc	1320
ctggcccata	tggaggccac	cggggtacgg	cgggacgtgg	cctaccttca	ggccctttcc	1380
ctggagcttg	cggaggagat	ccgccgcctc	gaggaggagg	tcttccgctt	ggcgggccac	1440
cccttcaacc	tcaactcccc	ggaccagctg	gaaaggggtg	tctttgacga	gcttaggctt	1500
ccgccttga	agaagacgaa	gaagacaggc	aagcgctcca	ccagcgcgcg	ggtgctggag	1560
gccctacggg	aggcccaccc	catcgtggag	aagatcctcc	agcaccggga	gctcaccaag	1620
ctcaagaaca	cctacgtgga	ccccctccca	agcctcgtcc	acccgaggac	gggcgcctc	1680
cacaccgcgt	tcaaccagac	ggccacggcc	acggggaggc	ttagtagctc	cgacccaac	1740
ctgcagaaca	tccccgtccg	cacccccttg	ggccagagga	tccgccgggc	cttcgtggcc	1800
gaggcgggtt	gggcgttggg	ggccctggac	tatagccaga	tagagctccg	cgtcctcgcc	1860
cacctctccg	gggacgaaaa	cctgatcagg	gtcttcagg	aggggaagga	catccacacc	1920
cagaccgcaa	gctggatggt	cggcgtcccc	ccggaggccg	tggaccccct	gatgcgcggg	1980
gcggccaaga	cgggtgaactt	cggcgtcctc	tacggcatgt	ccgcccatag	gctctcccag	2040
gagcttgcca	tcccctacga	ggaggcggtg	gcctttatag	agcgctactt	ccaaagcttc	2100
cccaaggtgc	gggcctggat	agaaaagacc	ctggaggagg	ggaggaagcg	gggctacgtg	2160

gaaaccctct tcggaagaag gcgctacgtg cccgacctca acgcccgggt gaagagcgtc	2220
agggaggccg cggagcgcat ggccttcaac atgcccgtcc agggcaccgc cgccgacctc	2280
atgaagctcg ccatggtgaa gctcttcccc cgctccggg agatgggggc ccgcatgctc	2340
ctccaggctcg ccaacgagct cctcctggag gccccccaag cgcgggccga ggaggtggcg	2400
gctttggcca aggaggccat ggagaaggcc tatccccctg ccgtgcccct ggaggtggag	2460
gtgggggatgg gggaggactg gctttccgcc aagggtcacc accaccacca ccac	2514

<210> 455

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 455

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggctcc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgcgc	420
atcctcaccg ccgaccgcga cctetaecaa ctcgctctcg accgcgtcgc cgctcctccac	480
cccgagggcc acctcatcac ccgggagtgg ctttgggaga agtatgggct taagccttcc	540
cagtgggtgg actaccgggc cttggccggg gacccttcg acaacatccc cggcgtgaag	600
ggcatcgggg agaagacggc ggccaagctg atccgggagt ggggaagcct ggaaaacctt	660
cttaagcacc tggaacaggt gaaacctgcc tccgtgcggg agaagatcct tagccacatg	720
gaggacctca agctatccct ggagctatcc cgggtgcaca cggacttgct ccttcagggtg	780
gacttcgccc ggcgcgggga gccggaccgg gaggggctta aggccttttt ggagaggctg	840
gagttcgga gctcctcca cgagttcggc ctggtggaaa gcccggtggc ggcggaggaa	900
gtccctggc cccccccga gggagccttc gtggggtacg ttctttcccg ccccgagccc	960
atgtgggcgg agcttaacgc cttggccgcc gcctggggcg gccgcgtgca ccgggcagca	1020
gacctcttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctcggtcccc gggacgaccc catgctcctc	1140

gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcgggc ctacgggggg	1200
gagtggacgg aggacgccc ccaccgggccc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc	1320
ctctccccggg tcctggccca tatggaggcc accggggtag ggcgggacgt ggcctacctt	1380
caggcccttt ccttgagct tgcggaggag atccgcccgc tcgaggagga ggtcttcgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac	1500
gagcttaggc ttcccgctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctacca agctcaagaa cacctacgtg gacccccctc caagcctcgt ccacccgagg	1680
acgggcccgc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgaccca acctgcagaa catccccgtc cgcaccccct tgggccagag gatccgcccg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag	1920
gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc	1980
ctgatgcgcc gggcgggcaa gacggtgaac ttcggcgtcc tctacggcat gtccgccccat	2040
aggtctctcc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100
ttccaaagct tccccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag	2160
cggggctacg tggaaacctc cttcggaaga aggcgctacg tgcccgacct caacgcccgg	2220
gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc	2280
gccgcgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg	2340
gcccgcatgc tcctccaggt cgccaacgag ctctctctgg agggccccca agcgcgggcc	2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc	2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac	2520
caccac	2526

<210> 456

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 456

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Lys	Pro	Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	195	200	205	
Lys	Leu	Ile	Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	210	215	220	
Glu	Gln	Val	Lys	Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	225	230	235	240
Glu	Asp	Leu	Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu	245	250	255	
Leu	Leu	Gln	Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	260	265	270	
Leu	Lys	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	275	280	285	
Phe	Gly	Leu	Leu	Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300	
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	305	310	315	320

Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Trp Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 457

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 457

ttccaggtgc ttgaggaggt tttccag

27

<210> 458

<211> 27

<212> DNA

<213> Artificial Sequence .

<220>

<223> Synthetic

<400> 458
ctcctcaagc acctggaaca ggtgaaa

27

<210> 459

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 459

atgaattccg aggcgatgct tccgctcttt gaaccctaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcc tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctaccaa ctctctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagcacc tggaaacagg gaaacctgcc tccgtgcggg agaagatcct tagccacatg	720
gaggacctca agctatccct ggagctatcc cgggtgcaca cggacttgct ccttcagggtg	780
gacttcgccc ggcgcggga gccggaccgg gaggggctta aggccttttt ggagaggctg	840
gagttcggaa gcctcctcca cgagttcggc ctgttgaaa gcccggtggc ggcggaggaa	900
gctccctggc cgcgcgcga gggagccttc gtggggtacg ttctttcccg ccccgagccc	960
atgtgggcgg agcttaacgc cttggccgcc gcctggggcg gccgcgtgca ccgggcagca	1020
gacccttggt cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttggt cctcgaggga ggggctagac ctctgcccc gggacgacct catgctctc	1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcgcg ctacgggggg	1200
gagtggacgg aggacgcgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc ctttggtct accacgaggt ggaaaagccc	1320
ctctcccggg tcctggcca tatggaggcc accggggtac ggcgggacgt ggctacctt	1380

caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc 1440
 ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac 1500
 gagcttaggc ttcccgctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc 1560
 gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620
 gagctcacca agctcaagaa cacctacgtg gacccccctcc caagcctcgt ccacccgagg 1680
 acgggcccgc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
 tccgacccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgccgg 1800
 gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
 cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag 1920
 gacatccaca cccagaccgc aagctggatg ttcggcgctc ccccgagggc cgtggacccc 1980
 ctgatgcgcc gggcgggccaa gacggtgaac ttcggcgctc tctacggcat gtccgcccac 2040
 aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
 ttccaaagct tccccaaagt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
 cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgacct caacgcccgg 2220
 gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgcccacc tcatgaaget cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gcccgcatgc tcctccaggt cgccaacgag ctctcctgg agggccccca agcgcggggc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
 caccac 2526

<210> 460

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 460

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60
Val Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu
210 215 220
Glu Gln Val Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met
225 230 235 240
Glu Asp Leu Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu
245 250 255
Leu Leu Gln Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly
260 265 270
Leu Lys Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
275 280 285
Phe Gly Leu Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro
290 295 300
Pro Pro Glu Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro
305 310 315 320
Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val
325 330 335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
340 345 350
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
355 360 365
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
370 375 380

Asp 385	Pro	Ser	Asn	Thr	Thr 390	Pro	Glu	Gly	Val	Ala 395	Arg	Arg	Tyr	Gly	Gly 400
Glu	Trp	Thr	Glu	Asp 405	Ala	Ala	His	Arg	Ala 410	Leu	Leu	Ser	Glu	Arg	Leu 415
His	Arg	Asn 420	Leu	Leu	Lys	Arg	Leu	Glu 425	Gly	Glu	Glu	Lys	Leu 430	Leu	Trp
Leu	Tyr	His 435	Glu	Val	Glu	Lys	Pro 440	Leu	Ser	Arg	Val	Leu 445	Ala	His	Met
Glu	Ala 450	Thr	Gly	Val	Arg	Arg 455	Asp	Val	Ala	Tyr	Leu 460	Gln	Ala	Leu	Ser
Leu 465	Glu	Leu	Ala	Glu	Glu 470	Ile	Arg	Arg	Leu	Glu 475	Glu	Glu	Val	Phe	Arg 480
Leu	Ala	Gly	His 485	Pro	Phe	Asn	Leu	Asn 490	Ser	Arg	Asp	Gln	Leu 495	Glu	Arg
Val	Leu	Phe 500	Asp	Glu	Leu	Arg	Leu	Pro 505	Ala	Leu	Lys	Lys	Thr 510	Lys	Lys
Thr	Gly	Lys 515	Arg	Ser	Thr	Ser	Ala 520	Ala	Val	Leu	Glu	Ala 525	Leu	Arg	Glu
Ala 530	His	Pro	Ile	Val	Glu	Lys 535	Ile	Leu	Gln	His	Arg 540	Glu	Leu	Thr	Lys
Leu 545	Lys	Asn	Thr	Tyr	Val 550	Asp	Pro	Leu	Pro	Ser 555	Leu	Val	His	Pro	Arg 560
Thr	Gly	Arg	Leu	His 565	Thr	Arg	Phe	Asn	Gln 570	Thr	Ala	Thr	Ala	Thr	Gly 575
Arg	Leu	Ser	Ser 580	Ser	Asp	Pro	Asn	Leu 585	Gln	Asn	Ile	Pro 590	Val	Arg	Thr
Pro	Leu	Gly 595	Gln	Arg	Ile	Arg	Arg 600	Ala	Phe	Val	Ala	Glu 605	Ala	Gly	Trp
Ala 610	Leu	Val	Ala	Leu	Asp 615	Tyr	Ser	Gln	Ile	Glu 620	Leu	Arg	Val	Leu	Ala
His 625	Leu	Ser	Gly	Asp 630	Glu	Asn	Leu	Ile	Arg	Val 635	Phe	Gln	Glu	Gly	Lys 640
Asp	Ile	His	Thr 645	Gln	Thr	Ala	Ser	Trp	Met 650	Phe	Gly	Val	Pro 655	Pro	Glu
Ala	Val	Asp 660	Pro	Leu	Met	Arg	Arg 665	Ala	Ala	Lys	Thr	Val	Asn 670	Phe	Gly
Val	Leu	Tyr 675	Gly	Met	Ser	Ala	His 680	Arg	Leu	Ser	Gln	Glu 685	Leu	Ala	Ile
Pro	Tyr 690	Glu	Glu	Ala	Val	Ala	Phe 695	Ile	Glu	Arg	Tyr 700	Phe	Gln	Ser	Phe
Pro 705	Lys	Val	Arg	Ala	Trp 710	Ile	Glu	Lys	Thr	Leu 715	Glu	Glu	Gly	Arg	Lys 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 461

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 461

gtccaggttc ttgaggaggt tttccag

27

<210> 462

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 462

ctcctcaaga acctggaccg ggtaaag

27

<210> 463

<211> 2532

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 463

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcg tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctaccaa ctcgctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccggac tcgctccggc gcaagataga ggcgacctc	720
gaggacctcc acctctcctt agacctggcc cgcctccgca ccgacctccc cctggagggtg	780
gactttaagg ccttgcgcg caggaccccc gacctggagg gcctgagggc ctttttgag	840
gagctggagt tcggaagcct cctccacgag ttccggcctc tgggagggga gaagccccgg	900
gaggaggccc cctggcccc gcccgagggg gccttcgtgg gcttcctcct tccccgcaag	960
gagcccatgt gggcggagct tctggccctg gcggcggcct cgggcggccg cgtgcaccgg	1020
gcagcagacc ccttggcggg gctaaaggac ctcaaggagg tccggggcct cctcgccaag	1080
gacctcgccg tcttggcctc gagggagggg ctagacctcg tgcccgggga cgaccccatg	1140
ctcctcgctt acctcctgga cccttcgaac accacccccg agggggtggc gcggcgctac	1200
gggggggagt ggacggagga cgcgcgccac cgggccctcc tctcgagag gctccatcgg	1260
aacctcctta agcgcctcga gggggaggag aagctccttt ggctctacca cgaggtggaa	1320
aagccccctt cccgggtcct ggcccatatg gagggcaccg gggtagggcg ggacgtggcc	1380
taccttcagg ccctttccct ggagcttgcg gaggagatcc gccgcctcga ggaggaggtc	1440
ttcgccttgg cgggccaccc cttcaacctc aactcccgg accagctgga aagggtgctc	1500
tttgacgagc ttaggcttcc cgccttgaag aagacgaaga agacaggcaa gcgctccacc	1560
agcgcgcggg tgctggaggc cctacgggag gccacccca tcgtggagaa gatcctccag	1620
caccgggagc tcaccaagct caagaacacc tacgtggacc ccctcccaag cctcgtccac	1680

ccgaggacgg gccgcctcca caccgccttc aaccagacgg ccacggccac ggggaggctt 1740
 agtagctccg accccaacct gcagaacatc cccgtccgca ccccttggg ccagaggatc 1800
 cgccgggcct tcgtggccga ggcgggttg gcgttggtgg ccctggacta tagccagata 1860
 gagctccgcg tctcgcacca cctctccggg gacgaaaacc tgatcagggt cttccaggag 1920
 gggaaggaca tccacacca gaccgcaagc tggatgttcg gcgtccccc ggaggccgtg 1980
 gacccctga tgcgccgggc ggccaagacg gtgaacttcg gcgtcctcta cggcatgtcc 2040
 gcccataggc tctcccagga gcttgccatc ccctacgagg aggcgggtggc ctttatagag 2100
 cgctacttcc aaagcttccc caaggtgcgg gcctggatag aaaagaccct ggaggagggg 2160
 aggaagcggg gctacgtgga aaccctcttc ggaagaaggc gctacgtgcc cgacctcaac 2220
 gcccggtga agagcgtcag ggaggccgcg gagcgcattg cttcaacat gcccgccag 2280
 ggcaccgccc cgcacctcat gaagctcgcc atggtgaagc tcttccccg cctccgggag 2340
 atggggggccc gcatgctcct ccaggtcgcc aacgagctcc tcctggaggc cccccaagcg 2400
 cgggccgagg aggtggcggc tttggccaag gaggccatgg agaaggccta tcccctcgcc 2460
 gtgccccctgg aggtggagggt ggggatgggg gaggactggc tttccgcaa gggtcaccac 2520
 caccaccacc ac 2532

<210> 464

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 464

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu
 225 230 235 240
 Glu Asp Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu
 260 265 270
 Glu Gly Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu
 275 280 285
 His Glu Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro
 290 295 300
 Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys
 305 310 315 320
 Glu Pro Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly
 325 330 335
 Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys
 340 345 350
 Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg
 355 360 365
 Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr
 370 375 380
 Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr
 385 390 395 400
 Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu
 405 410 415
 Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu
 420 425 430

Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala
 435 440 445
 His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala
 450 455 460
 Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val
 465 470 475 480
 Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu
 485 490 495
 Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr
 500 505 510
 Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu
 515 520 525
 Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu
 530 535 540
 Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His
 545 550 555 560
 Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala
 565 570 575
 Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val
 580 585 590
 Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala
 595 600 605
 Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val
 610 615 620
 Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu
 625 630 635 640
 Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro
 645 650 655
 Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn
 660 665 670
 Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu
 675 680 685
 Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln
 690 695 700
 Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly
 705 710 715 720
 Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val
 725 730 735
 Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg
 740 745 750
 Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys
 755 760 765

Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg
 770 775 780

Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala
 785 790 795 800

Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala
 805 810 815

Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp
 820 825 830

Trp Leu Ser Ala Lys Gly His His His His His His
 835 840

<210> 465

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 465
 gacgtccttc ggggtgatga ggtggcc

27

<210> 466

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 466
 atcaccccgaggacgtcca ggagaag

27

<210> 467

<211> 2532

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 467

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttccg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg ttaccgcgc tcgagggtccc cggtacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgcgc	420
atcctcaccg ccgaccgga cctctacca ctcgtctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac ccgaaggac gtccaggaga agtacggggg gccccggag	540
cgctgggtgg acttccgcgc cctcacgggg gaccgctcgg acaacatccc cggggtggcg	600
gggatagggg agaagaccgc cttcgactc ctgcagagt gggggagcgt ggaaaacctc	660
ctgaagaacc tggaccgggt aaagccggac tcgctccggc gcaagataga ggcgacctc	720
gaggacctcc acctctcctt agacctggcc cgcctccgca ccgacctccc cctggagggtg	780
gactttaagg ccctgcgcg caggaccccc gacctggagg gcctgagggc ctttttggag	840
gagctggagt tcggaagcct cctccacgag ttccggcctcc tgggagggga gaagccccgg	900
gaggaggccc cctggcccc gcccgaaggg gccttcgtgg gcttctcctt tccccgaag	960
gagcccatgt gggcgagct tctggccctg gggcgggcct cggcgggccg cgtgcaccg	1020
gcagcagacc ccttggcggg gctaaaggac ctcaaggagg tccggggcct cctcgccaag	1080
gacctcgccg tcttggcctc gaggagggg ctagacctcg tgcccgggga cgaccccatg	1140
ctcctcgctt acctcctgga cccttcgaac accacccccg aggggggtggc gggcgctac	1200
gggggggagt ggacggagga cgcgcccac cgggcccctc tctcgagag gctccatcgg	1260
aacctcctta agcgctcga ggggaggag aagctccttt ggctctacca cgagggtgaa	1320
aagccccctt cccgggtcct ggcccatatg gaggccaccg gggtagggcg ggacgtggcc	1380
taccttcagg ccctttccct ggagcttgcg gaggagatcc gccgcctcga ggaggaggtc	1440
ttccgcttgg cgggccacc cttcaacctc aactcccggg accagctgga aagggtgctc	1500
tttgacgagc ttaggcttcc cgccttgaag aagacgaaga agacaggcaa gcgtccacc	1560
agcgccgcgg tgctggaggc cctacgggag gccacccca tcgtggagaa gatcctccag	1620
caccgggagc tcaccaagct caagaacacc tacgtggacc ccctcccaag cctcgtccac	1680
ccgaggacgg gccgcctcca caccgcttc aaccagacgg ccacggccac ggggaggctt	1740
agtagctccg accccaacct gcagaacatc cccgtccgca ccccttggg ccagaggatc	1800
cgccgggcct tcgtggccga ggcgggttgg gcgttggtgg ccctggacta tagccagata	1860

gagctccgcg tcctcgccca cctctccggg gacgaaaacc tgatcagggt cttccaggag 1920
 gggaaggaca tccacaccca gaccgcaagc tggatgttcg gcgtccccc ggaggccgtg 1980
 gacccctga tgcgccgggc ggccaagacg gtgaacttcg gcgtcctcta cggcatgtcc 2040
 gcccataggc tctcccagga gcttgccatc ccctacgagg aggcggtggc ctttatagag 2100
 cgctacttcc aaagcttccc caaggtgcgg gcctggatag aaaagaccct ggaggagggg 2160
 aggaagcggg gctacgtgga aacctcttc ggaagaaggc gctacgtgcc cgacctcaac 2220
 gcccggtga agagcgtcag ggaggccgcg gagcgcatgg cttcaacat gcccgccag 2280
 ggcaccgccg ccgacctcat gaagctcgcc atggtgaagc tcttcccccg cctccgggag 2340
 atggggggccc gcatgctcct ccaggtcgcc aacgagctcc tctggaggc cccccaagcg 2400
 cgggccgagg aggtggcggc tttggccaag gaggccatgg agaaggccta tcccctcgcc 2460
 gtgcccctgg aggtggagggt ggggatgggg gaggactggc tttccgcaa gggtcaccac 2520
 caccaccacc ac 2532

<210> 468

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 468

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
			85					90						95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
		100					105						110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160
 Pro Glu Gly His Leu Ile Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly
 165 170 175
 Val Pro Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg
 180 185 190
 Ser Asp Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205
 Arg Leu Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu
 210 215 220
 Asp Arg Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu
 225 230 235 240
 Glu Asp Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu
 260 265 270
 Glu Gly Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu
 275 280 285
 His Glu Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro
 290 295 300
 Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys
 305 310 315 320
 Glu Pro Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly
 325 330 335
 Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys
 340 345 350
 Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg
 355 360 365
 Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr
 370 375 380
 Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr
 385 390 395 400
 Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu
 405 410 415
 Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu
 420 425 430
 Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala
 435 440 445
 His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala
 450 455 460

Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val
 465 470 475 480
 Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu
 485 490 495
 Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr
 500 505 510
 Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu
 515 520 525
 Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu
 530 535 540
 Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His
 545 550 555 560
 Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala
 565 570 575
 Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val
 580 585 590
 Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala
 595 600 605
 Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val
 610 615 620
 Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu
 625 630 635 640
 Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro
 645 650 655
 Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn
 660 665 670
 Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu
 675 680 685
 Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln
 690 695 700
 Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly
 705 710 715 720
 Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val
 725 730 735
 Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg
 740 745 750
 Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys
 755 760 765
 Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg
 770 775 780
 Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala
 785 790 795 800

Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala
805 810 815
Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp
820 825 830
Trp Leu Ser Ala Lys Gly His His His His His His
835 840

<210> 469

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 469

ctcgaggcgg gtaaacccca ggaggtc

27

<210> 470

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 470

gggtttaccg gcctcgaggt gcccggc

27

<210> 471

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 471

atgaattccg aggcgatgct tccgctcttt gaaccctaaag gccgggtcct cctggtggac

60

ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc

120

gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac

180

gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc

240

tacgaggcct acaaggcggg gagggcccg acccccgagg acttcccccg gcagctcgcc

300

ctcatcaagg agctggtgga cctcctggggg tttacccgcc tgcaggtgcc gggctttgaa	360
gcggatgacg tcctggctac cctggccaag aaggcggaaa aggaaggcta cgaagtgcgc	420
atcctcaccg cggaccggga cctttaccag cttcttttcgg agcgaatctc catccttcac	480
ccggagggtt acctgatcac cccggagtgg ctttgggaga agtatgggct taagccttcc	540
cagtgggtgg actaccgggc cttggccggg gacccttcgg acaacatccc cggcgtgaag	600
ggcatcgggg agaagacggc ggccaagctg atccgggagt ggggaagcct ggaaaacctt	660
cttaagcacc tggaacaggt gaaacctgcc tccgtgcggg agaagatcct tagccacatg	720
gaggacctca agctatccct ggagctatcc cgggtgcaca cggacttgct ccttcaggtg	780
gacttcgccc ggcgccggga gccggaccgg gaggggctta aggccttttt ggagaggctg	840
gagttcgga gctcctcca cgagttcggc ctgttgaaa gcccgggtggc ggcggaggaa	900
gctccctggc cccccccga gggagccttc gtggggtagc ttctttcccg ccccgagccc	960
atgtgggcgg agcttaacgc cttggccgcc gcctggggcg gccgcgtgca ccgggcagca	1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctcgtagccc gggacgaccc catgctcctc	1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcgcg ctacgggggg	1200
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc ctttggtctt accacgaggt ggaaaagccc	1320
ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccttgagct tgcggaggag atccgccgc tcgaggagga ggtcttcgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaaggg gctctttgac	1500
gagcttaggc ttccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggcctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctcacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg	1680
acgggcccgc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgaccca acctgcagaa catcccgc cgcacccct tgggccagag gatccgccg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag	1920
gacatccaca cccagaccgc aagctggatg ttcggcgctc ccccgaggc cgtggacccc	1980
ctgatgcgc gggcgggcaa gacggtgaac ttcggcgctc tctacggcat gtccgccat	2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100
ttccaaagct tcccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag	2160

cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgcacct caacgcccgg 2220
 gtgaagagcg tcagggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gcccgcatgc tcctccaggt cgccaacgag ctctccttgg agggccccca agcgcggggc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
 caccac 2526

<210> 472

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 472

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	145	150	155	160

Pro Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175
 Leu Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro
 180 185 190
 Ser Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala
 195 200 205
 Lys Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu
 210 215 220
 Glu Gln Val Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met
 225 230 235 240
 Glu Asp Leu Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu
 245 250 255
 Leu Leu Gln Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Lys Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 473

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 473

aagccactcc ggggtgatca ggtaacc

27

<210> 474

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 474

atcaccccgagggtggctttg ggagaag

27

<210> 475

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 475

atgaattccc tgcccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac

60

ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc

120

caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg

180

gtgatcgtgg tctttgacgc cgaggccccc tccttccgcc accagacctt cgaggcctac

240

aaggcggggc gggctccac ccccgaggac tttcccggc agcttgcct tatcaaggag

300

atggtggacc	ttttgggcct	ggagcgcctc	gaggtgccgg	gctttgaagc	ggatgacgtc	360
ctggctaccc	tggccaagaa	ggcggaaaag	gaaggctacg	aagtgcgcat	cctcaccgcg	420
gaccgggacc	tttaccagct	tctttcggag	cgaatctcca	tccttcaccc	ggaggggttac	480
ctgatcacc	cggagtggct	ttgggagaag	tacggcctca	ggccggagca	gtgggtggac	540
ttccgcgccc	tcgtggggga	cccctccgac	aacctccccg	gggtcaaggg	catcggggag	600
aagaccgccc	tcaagctcct	caaggagtgg	ggaagcctgg	aaaacctcct	caagaacctg	660
gaccgggtaa	agccagaaaa	cgtccgggag	aagatcaagg	cccacctgga	agacctcagg	720
ctctccttgg	agctctcccc	ggtgcgcacc	gacctcccc	tggaggtgga	cctcgcgccag	780
gggcgggagc	ccgaccggga	ggggcttagg	gccttcctgg	agaggctgga	gttcggcagc	840
ctcctccacg	agttcggcct	cctggaggcc	cccgcctccc	tggaggaggc	cccctggccc	900
ccgccggaag	gggccttcgt	gggcttcgtc	ctctcccgcc	ccgagcccat	gtgggcggag	960
cttaaagccc	tggccgcctg	caggggcggc	cgcgtcgacc	gggcagcaga	ccccttgggc	1020
gggctaaagg	acctcaagga	ggtccggggc	ctcctcgcca	aggacctcgc	cgtcttgggc	1080
tcgagggagg	ggctagacct	cgtgcccggg	gacgaccca	tgtcctcgc	ctacctctg	1140
gacccttcga	acaccacccc	cgaggggggtg	gcgcggcgct	acggggggga	gtggacggag	1200
gacgccgccc	accggggcct	cctctcgag	aggctccatc	ggaacctcct	taagcgctc	1260
gagggggagg	agaagctcct	ttggctctac	cacgaggtgg	aaaagcccct	ctcccggtc	1320
ctggcccata	tggaggccac	cggggtacgg	cgggacgtgg	cctaccttca	ggccctttcc	1380
ctggagcttg	cggaggagat	ccgccgcctc	gaggaggagg	tcttcgctt	ggcgggccac	1440
cccttcaacc	tcaactccc	ggaccagctg	gaaaggggtg	tctttgacga	gcttaggctt	1500
ccgccttga	agaagacgaa	gaagacaggc	aagcgctcca	ccagcgccgc	ggtgctggag	1560
gccctacggg	aggcccaccc	catcgaggag	aagatcctcc	agcaccggga	gctcaccaag	1620
ctcaagaaca	cctacgtgga	ccccctcca	agcctcgctc	acccgaggac	gggcgcgctc	1680
cacaccgcgt	tcaaccagac	ggccacggcc	acggggaggc	ttagtagctc	cgaccccaac	1740
ctgcagaaca	tccccgtccg	caccccttg	ggccagagga	tccgccgggc	cttcgtggcc	1800
gaggcgggtt	gggcgttgg	ggccctggac	tatagccaga	tagagctccg	cgtcctcgcc	1860
cacctctccg	gggacgaaaa	cctgatcagg	gtcttcagg	aggggaagga	catccacacc	1920
cagaccgcaa	gctggatgtt	cggcgtcccc	cggaggccg	tggacccct	gatgcgccgg	1980
gcggccaaga	cgggtgaactt	cggcgtcctc	tacggcatgt	ccgccatag	gctctcccag	2040
gagcttgcca	tcccctacga	ggaggcgggtg	gcctttatag	agcgctactt	ccaaagcttc	2100
cccaaggtgc	gggcctggat	agaaaagacc	ctggaggagg	ggaggaagcg	gggctacgtg	2160

gaaaccctct tcggaagaag gcgctacgtg cccgacctca acgcccgggt gaagagcgtc 2220
 agggaggccg cggagcgcat ggccttcaac atgcccgtcc agggcaccgc cgccgacctc 2280
 atgaagctcg ccatggtgaa gctcttcccc cgctccggg agatgggggc ccgcatgctc 2340
 ctccaggctg ccaacgagct cctcctggag gccccccaag cgcgggccga ggaggtggcg 2400
 gctttggcca aggaggccat ggagaaggcc tatccccctcg ccgtgcccct ggaggtggag 2460
 gtggggatgg gggaggactg gctttccgcc aagggtcacc accaccacca ccac 2514

<210> 476

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 476

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	1	5	10	15
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu	20	25	30	
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu	130	135	140	
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr	145	150	155	160
Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Glu	165	170	175	
Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp	Asn	Leu	180	185	190	

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu Leu Lys
 195 200 205
 Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val Lys
 210 215 220
 Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp Leu Arg
 225 230 235 240
 Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val
 245 250 255
 Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg Ala Ala
 325 330 335
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
 405 410 415
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
 450 455 460
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525

Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
530 535 540
Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
545 550 555 560
His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
565 570 575
Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
580 585 590
Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala
595 600 605
Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
610 615 620
Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr
625 630 635 640
Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
645 650 655
Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly
660 665 670
Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
675 680 685
Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
690 695 700
Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val
705 710 715 720
Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
725 730 735
Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
740 745 750
Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
755 760 765
Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala
770 775 780
Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala
785 790 795 800
Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro
805 810 815
Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
820 825 830
His His His His His His
835

<210> 477
 <211> 64
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 477
 caccaccacc accaccacgt cgactagtgc tagcgtcgac tagctgcagg catgcaagct 60
 tggc 64
 <210> 478
 <211> 64
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 478
 gccaaagcttg catgcctgca gctagtcgac gctagcacta gtcgacgtgg tggtggtggt 60
 ggtg 64
 <210> 479
 <211> 41
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 479
 caggaagcgg ccgcgtcgac atgaccatga ttacgccaaag c 41
 <210> 480
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 480
 gggcccgcca gggtcgactc agggcgatgg cccactacgt ga 42
 <210> 481
 <211> 3135
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 481
 atgaattccg aggcgatgct tccgctcttt gaacccaaaag gccgggtcct cctgggtggac 60
 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
 gaaccgggtgc aggcgggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
 ggggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgc ccacgaggcc 240
 tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300
 ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag 360
 gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgcgc 420
 atcctcaccg ccgaccgca cctctaccaa ctctctccg accgcgtcgc cgtcctccac 480
 cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
 cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cgggggtcaag 600
 ggcacgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
 ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
 gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
 gacctcgccc aggggaggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
 gaggtcggca gcctcctcca cgagttcggc ctctggagg ccccgcccc cctggaggag 900
 gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc 960
 atgtgggcgg agcttaaagc cctggccgcc tgcaggggag gccgcgtgca ccgggcagca 1020
 gacctcttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
 gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgacct catgctcctc 1140
 gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgggcg ctacgggggg 1200
 gaggggacgg aggacggcg ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260
 cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc 1320
 ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggctacctt 1380

caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac	1500
gagcttaggc ttcccgctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctcacca agctcaagaa cacctacgtg gacccccctc caagcctcgt ccacccgagg	1680
acggggccgcc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgaccca acctgcagaa catccccgtc cgcacccct tgggccagag gatccgccgg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggcttcca ggaggggaag	1920
gacatccaca ccagaccgc aagctggatg ttcggcgctc ccccgaggc cgtggacccc	1980
ctgatgcgcc gggcgggcaa gacggtgaac ttcggcgctc tctacggcat gtccgcccac	2040
aggctctccc aggagcttgc catccccctac gaggaggcgg tggcctttat agagcgctac	2100
ttccaaagct tcccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag	2160
cggggctacg tggaaaccct cttcggaaga aggcgtacg tgcccgacct caacgcccgg	2220
gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc	2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg	2340
gcccgcacgc tcttcaggt cgccaacgag ctctcctcgg agggccccca agcgcggggc	2400
gaggagggtg cggttttggc caaggaggcc atggagaagg cctatccccct cgccgtgccc	2460
ctggagggtg aggtggggat gggggaggac tggctttccg ccaagggtea ccaccaccac	2520
caccacgtcg acatgaccat gattacgcca agctatcttag gtgacactat agaatactca	2580
agctatgcat caagcttggg accgagctcg gatccactag taacggccgc cagtgtgctg	2640
gaattctgca gatatccatc acactggcgg ccgctcgagc atgcatctag agggcccaat	2700
tcgccctata gtgagtcgta ttacaattca ctggccgctg ttttacaacg tcgtgactgg	2760
gaaaaccctg gcgttaccca acttaatcgc cttgcagcac atcccccttt cgccagctgg	2820
cgtaatagcg aagaggcccg caccgatcgc ccttcccaac agttgcgcag cctgaatggc	2880
gaatgggacg cgccctgtag cggcgcatta agcgcggcgg gtgtgggtgg tacgcgcagc	2940
gtgaccgcta cacttgccag cgccctagcg ccgctcctt tcgctttctt cccttccttt	3000
ctcgccacgt tcgccgctt tccccgtaa gctctaaatc gggggctccc tttagggttc	3060
cgatttagag ctttacggca cctcgaccgc aaaaaacttg atttgggtga tggttcacgt	3120
agtgggcat cgccc	3135

<210> 482

<211> 1045

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 482

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	
1				5					10					15		
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	
			20					25					30			
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	
		35					40					45				
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	
	50					55					60					
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	
65					70					75					80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	
				85					90					95		
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	
			100					105					110			
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	
		115					120					125				
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	
	130					135					140					
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	
145					150				155						160	
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	
				165					170					175		
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	
			180					185					190			
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	
		195					200					205				
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	
	210					215					220					
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	
225					230					235					240	
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	
				245					250					255		

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His Val Asp Met Thr Met Ile
 835 840 845
 Thr Pro Ser Tyr Leu Gly Asp Thr Ile Glu Tyr Ser Ser Tyr Ala Ser
 850 855 860
 Ser Leu Val Pro Ser Ser Asp Pro Leu Val Thr Ala Ala Ser Val Leu
 865 870 875 880
 Glu Phe Cys Arg Tyr Pro Ser His Trp Arg Pro Leu Glu His Ala Ser
 885 890 895
 Arg Gly Pro Asn Ser Pro Tyr Ser Glu Ser Tyr Tyr Asn Ser Leu Ala
 900 905 910
 Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
 915 920 925

Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu
 930 935 940
 Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly
 945 950 955 960
 Glu Trp Asp Ala Pro Cys Ser Gly Ala Leu Ser Ala Ala Gly Val Val
 965 970 975
 Val Thr Arg Ser Val Thr Ala Thr Leu Ala Ser Ala Leu Ala Pro Ala
 980 985 990
 Pro Phe Ala Phe Phe Pro Ser Phe Leu Ala Thr Phe Ala Gly Phe Pro
 995 1000 1005
 Arg Gln Ala Leu Asn Arg Gly Leu Pro Leu Gly Phe Arg Phe Arg
 1010 1015 1020
 Ala Leu Arg His Leu Asp Arg Lys Lys Leu Asp Leu Gly Asp Gly
 1025 1030 1035
 Ser Arg Ser Gly Pro Ser Pro
 1040 1045

<210> 483

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 483

cgggacctcg aggcgcgtga accccaggag gtccac

36

<210> 484

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 484

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc	60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag	120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggcctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggcccgggc cccacgccg gaggactttc cccggcaact cgcctcatc	300

aaggagctgg	tggacctcct	ggggttcacg	cgcctcgagg	tcccgggcta	cgaggcggac	360
gacgtcctgg	ccagcctggc	caagaaggcg	gaaaaggagg	gctacgaggt	ccgcatacctc	420
accgccgaca	aagaccttta	ccagctcctt	tccgaccgca	tccacgtcct	ccacccccgag	480
gggtacctca	tcacccccggc	ctggcctttg	gaaaagtacg	gcctgaggcc	cgaccagtgg	540
gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccgggggt	caagggcatc	600
ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
aagctctcct	gggacctggc	caaggtgcg	accgacctgc	ccctggaggt	ggacttcgcc	780
aaaaggcggg	agccccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggccccctgg	900
cccccgccgg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtggggc	960
gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agacccttg	1020
gcggggctaa	aggacctcaa	ggaggtcggg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgcctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgcggc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cggcgggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
cacccttca	acctcaactc	ccgggaccag	ctggaaaggg	tgctctttga	cgagcttagg	1500
cttcccgcct	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcgtg	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccccctc	ccaagcctcg	tccacccgag	gacgggccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttgggccaga	ggatccgccg	ggccttcgtg	1800
gccgaggcgg	ggtgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gcccacctct	ccggggacga	aaacctgac	agggctctcc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgctc	cccccgagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agacggtgaa	cttcggcgctc	ctctacggca	tgtccgcca	taggctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100
ttccccaagg	tgcgggcctg	gatagaaaag	accctggagg	aggggaggaa	gcggggctac	2160

gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgcccg ggtgaagagc 2220
 gtcagggagg ccgcgaggcg catggccttc aacatgcccg tccagggcac cgccgcccac 2280
 ctcataaagc tcgcatggt gaagctcttc ccccgccctcc gggagatggg ggcccgcagc 2340
 ctcctccagg tcgccaacga gctcctcctg gagggccccc aagcgcgggc cgaggaggtg 2400
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 485

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 485

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 486

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 486

gtggaccttc tgggctttac ccgcctcgag gccccg

36

<210> 487

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 487

cggggcctcg aggcgggtaa agcccagaag gtccac

36

<210> 488

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 488

Met Asn Ser Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu
20 25 30

Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe
35 40 45

Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
 100 105 110
 Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys
 115 120 125
 Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg
 130 135 140
 Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp
 145 150 155 160
 Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro
 165 170 175
 Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp
 180 185 190
 Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu
 195 200 205
 Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp
 225 230 235 240
 Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830

Ser Ala Lys Gly His His His His His His
 835 840

<210> 489

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 489

tttaccgcgcc tcgaggtgcc gggc

24

<210> 490

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 490

cggcacctcg aggcgggtaa agcccaaaag gtccac

36

<210> 491

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 491

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	1	5	10	15
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu	20	25	30	
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu	130	135	140	
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr	145	150	155	160
Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser	165	170	175	
Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile	180	185	190	
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile	Arg	195	200	205	
Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val	Lys	210	215	220	
Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu	Lys	225	230	235	240
Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu	Leu	Leu	Gln	Val	245	250	255	
Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala	Phe	260	265	270	
Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	275	280	285	
Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	290	295	300	
Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	305	310	315	320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala
 325 330 335
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
 405 410 415
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
 450 455 460
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540
 Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr
 625 630 635 640
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
 645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 755 760 765
 Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala
 770 775 780
 Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala
 785 790 795 800
 Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro
 805 810 815
 Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
 820 825 830
 His His His His His His
 835

<210> 492

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 492

atcgtggtct ttgacgccga ggccccctcc ttcc

34

<210> 493

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 493
ggaaggagg ggcctcggcg tcaaagacca cgat

34

<210> 494

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 494

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	210	215	220	
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	225	230	235	240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 495

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 495
atgaattcgg ggatgctgcc cctctttgag cccaagggcc ggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cggggccgggc cccacgccc gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caaggtgccc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg cttcttgga agccccaagg ccctggagga ggccccctgg 900
ccccgcgcgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agaccccttg 1020
gcgggggctaa aggacctcaa ggaggtcggg ggcctcctcg ccaaggacct cgccgtcttg 1080
gcctcgaggg aggggctaga cctcgtgcc ggggacgacc ccatgctcct cgctacctc 1140
ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200
gaggacgccc cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380
tccttgagc ttgaggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500
cttccgcct tgaagaagac gaagaagaca ggcaagcgt ccaccagcgc cgcggtgctg 1560
gaggccctac gggaggccca cccatcgtg gagaagatcc tcacgaccg ggagctcacc 1620
aagctcaaga acacctacgt ggacccctc ccaagcctcg tccacccgag gacgggccgc 1680
ctccacacc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740
aacctgcaga acatccccgt ccgcacccc ttgggccaga ggatccgccg ggccttcgtg 1800
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860

gccacacctt cccggggacga aaacctgatc aggggtcttcc aggaggggaa ggacatccac 1920
 acccagaccg caagctggat gttcggcgtc cccccggagg ccgtggaccc cctgatgcgc 1980
 cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc 2040
 caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100
 ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
 gtggaaaacc tcttcggaag aaggcgctac gtgcccagacc tcaacgcccg ggtgaagagc 2220
 gtcaggaggc ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tcgccatggt gaagctcttc cccgcctcc gggagatggg ggcccgcgac 2340
 ctctccagg tcgccaacga gtcctcctg gagggccccc aagcgcgggc cgaggagggtg 2400
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 496

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 496

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35				40						45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50				55						60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65				70					75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85					90						95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Gly His His His His His His
835

<210> 497

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 497

```

atgaattcca ccccaactttt tgacctggag gaacccccca agcgggtgct tctggtggac      60
ggccaccacc tggcctaccg caccttctat gccctgagcc tcaccacctc ccgggggggag      120
ccggtgcaga tgggtctacgg cttcgcccgg agcctcctca aggccttgaa ggaggacgga      180
caggcgggtg tegtgtgtct tgacgcccag gccccctcct tccgccacga ggcctacgag      240
gcctacaagg cgggcccggc ccccaacccc gaggacttcc ccgccagct cgccttggtc      300
aagcggctgg tggaccttct gggcctggtc cgcctcgagg ccccggggta cgaggcggac      360
gacgtcctgg gcacctggc caagaaggcc gaaagggagg ggatggaggt gcgcacctc      420
acgggagacc gggacttctt ccagctcctc tccgagaagg tctcggctct cctgccggac      480
gggaccttgg tcaccccaaa ggacgtccag gagaagtacg gggtgcccc ggagcgctgg      540
gtggacttcc gcgcctcac gggggaccgc tcggacaaca tccccgggtt ggcggggata      600
ggggagaaga ccgcccttcg actcctcgca gagtggggga gcgtggaaaa cctcctgaag      660
aacctggacc gggtaaagcc ggactcgctc cggcgcaaga tagaggcgca cctcgaggac      720
ctccacctct ccttagacct gggccgcac cgcaccgacc tccccctgga ggtggacttt      780
aaggccctgc gccgcaggac ccccgacctg gagggcctga gggccttttt ggaggagctg      840
gagttcggaa gcctcctcca cgagttcggc ctcttgggag gggagaagcc ccgggaggag      900
gccccctggc ccccgccccg aggggccttc gtgggcttcc tcctttcccg caaggagccc      960
atgtggggcg agcttctggc cctggcgggc gcctcggggc gccgcgtgca ccgggcagca     1020
gacctcttgg cgggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc     1080
gccgtcttgg cctcgaggga ggggctagac ctctgtcccc gggacgacct catgctcctc     1140
gcctacctcc tggaccttcc gaacaccacc cccgaggggg tggcgcgggc ctacgggggg     1200
gagtggacgg aggacgcgcg ccaccgggccc ctctctcgg agaggctcca tcggaacctc     1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc     1320

```

ctctcccg	gg tcttg	gcccc	tatgg	aggcc	accgg	ggtac	ggcgg	gacgt	ggcct	acctt	1380			
caggcc	cttt ccctg	gagct	tg	cg	gaggag	atccg	ccgcc	tcg	aggagga	ggtct	tcgc	1440		
ttggc	ggggcc	accctt	caa cctca	actcc	cggg	accagc	tggaa	aggg	gtctt	ttgac	1500			
gagct	taggc	ttccgc	ctt gaaga	agacg	aaga	agacag	gcaag	cgctc	caccag	cgcc	1560			
gcggt	gctgg	aggcc	tacg	ggagg	ccac	cccat	cg	tgg	agaag	atcct	ccagc	accgg	1620	
gagct	cacca	agctc	aagaa	cacct	acgtg	gacccc	ctcc	caagc	ctcgt	ccaccc	gagg	1680		
acggg	ccgcc	tccac	acccg	cttca	accag	acggc	cacgg	ccacg	gggag	gcttag	tagc	1740		
tccg	accca	acctg	cagaa	catccc	cg	tcc	cg	acccc	ct	tggg	ccagag	gatcc	gcgg	1800
gcctt	cg	tgg	ccggg	ggg	gtgg	ccctg	actat	agcca	gatag	agctc	1860			
cg	gtc	ctcg	cccac	ctc	cgggg	acgaa	aacct	gatca	gggt	cttcca	ggagg	ggaag	1920	
gacat	ccaca	cccag	accgc	aagct	ggatg	ttcgg	cg	tcc	ccccg	gaggc	cg	tgg	acccc	1980
ctgat	gcgcc	gggcg	gcca	gacgg	tgaac	ttcgg	cg	tcc	tctac	ggcat	gtccg	cccat	2040	
aggct	ctccc	aggag	cttgc	catccc	ctac	gaggag	gcgg	tggc	ctttat	agagc	gctac	2100		
ttcaa	agct	tccca	aggt	gcggg	cctg	atagaa	aaga	ccctg	gagga	gggag	ggaag	2160		
cgggg	ctacg	tggaa	accct	cttcg	gaaga	aggc	gctacg	tggcc	gac	ct	caacg	ccccg	2220	
gtga	agagcg	tcagg	gaggc	cg	cg	gagcg	atggc	cttca	acatg	cccgt	ccagg	gcacc	2280	
gccgc	cgacc	tc	atga	agct	cgccat	ggtg	aagct	cttcc	cccgc	ctccg	ggagat	gggg	2340	
gccc	gcatgc	tctc	caggt	cgcca	acgag	ctc	ctc	ctg	aggc	ccccca	agcg	cgggcc	2400	
gaggag	ggtgg	cggct	ttggc	caagg	aggcc	atgg	agaagg	cctat	ccccct	cgccg	tggcc	2460		
ctggag	ggtgg	aggtg	ggggat	ggggg	aggac	tggc	tttccg	ccaagg	gtca	ccacc	accac	2520		
caccac												2526		

<210> 498

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 498

Met	Asn	Ser	Thr	Pro	Leu	Phe	Asp	Leu	Glu	Glu	Pro	Pro	Lys	Arg	Val
1				5					10					15	

Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Tyr	Ala	Leu
			20					25					30		

Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe
 35 40 45
 Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val
 50 55 60
 Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
 65 70 75 80
 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu
 100 105 110
 Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys
 115 120 125
 Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg
 130 135 140
 Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp
 145 150 155 160
 Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro
 165 170 175
 Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp
 180 185 190
 Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu
 195 200 205
 Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp
 225 230 235 240
 Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly His His His His His His
 835 840

<210> 499

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 499

atgaattccc tgccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac	60
ctggcctacc gtacctttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc	120
caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tctttgacgc cgaggcccc tccttcgcgc accagacctt cgaggcctac	240
aaggcggggc gggctccac ccccgaggac tttcccgcgc agcttgccct tatcaaggag	300
atggtggacc ttttggcct ggagcgctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcat cctcaccgcg	420
gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggagggttac	480
ctgatcacc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac	540
taccgggcct tggccgggga cccttcgcgc aacatccccg gcgtgaagg catcggggag	600
aagacggcgg ccaagctgat ccgggagtg ggaagcctgg aaaaccttct taagcacctg	660

gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag	720
ctatccctgg agctatcccc ggtgcacacg gacttgctcc ttcaggtgga cttcgccccg	780
cgccgggagc cggaccggga ggggcttaag gccttttttg agaggctgga gttcggaagc	840
ctcctccacg agttcggcct gttggaaagc ccggtggcgg cggaggaagc tccctggccg	900
cccccgagg gagccttcgt ggggtacgtt ctttcccgcc ccgagcccat gtgggcggag	960
cttaacgcct tggccgccgc ctggggcggc cgctgcacc gggcagcaga ccccttggcg	1020
gggctaaagg acctcaagga ggtccggggc ctctcgcga aggacctcgc cgtcttggcc	1080
tcgagggagg ggctagacct cgtgcccggg gacgaccca tgctcctcgc ctacctctg	1140
gaccttcga acaccacccc cgaggggggtg gcgcggcgct acggggggga gtggacggag	1200
gacgccgcc accgggcccct cctctcggag aggtccatc ggaacctcct taagcgcctc	1260
gagggggagg agaagctcct ttggctctac cacgaggtgg aaaagcccct ctcccggtc	1320
ctggcccata tggaggccac cggggtagcg cgggacgtgg cctaccttca ggccctttcc	1380
ctggagcttg cggaggagat ccgccgcctc gaggaggagg tcttcgcctt ggccggccac	1440
cccttcaacc tcaactcccg ggaccagctg gaaaggggtg tctttgacga gcttaggctt	1500
ccgccttga agaagacgaa gaagacaggc aagcgctcca ccagcggcgc ggtgctggag	1560
gccctacggg agggccaccc catcgtggag aagatcctcc agcaccggga gctcaccaag	1620
ctcaagaaca cctacgtgga cccctccca agcctcgtcc acccgaggac gggccgcctc	1680
cacaccgct tcaaccagac ggccacggcc acggggaggc ttagtagctc cgacccaac	1740
ctgcagaaca tccccgtccg ccccccttg ggccagagga tccgccgggc cttcgtggcc	1800
gaggcgggtt gggcgttggt ggccctggac tatagccaga tagagctccg cgtcctcgcc	1860
cacctctccg gggacgaaaa cctgatcagg gtcttcagg aggggaagga catccacacc	1920
cagaccgcaa gctggatggt cggcgctccc ccggaggccg tggaccccct gatgcgccgg	1980
gcggccaaga cggatgaactt cggcgctcctc tacggcatgt ccgccatag gctctcccag	2040
gagcttgcca tccctacga ggaggcgggt gcctttatag agcgctactt ccaaagcttc	2100
cccaagggtg gggcctggat agaaaagacc ctggaggagg ggaggaagcg gggctacgtg	2160
gaaacctct tcggaagaag gcgctacgtg cccgacctca acgcccgggt gaagagcgtc	2220
agggaggccg cggagcgcac ggcttcaac atgccgtcc agggcaccgc cgccgacctc	2280
atgaagctcg ccatggtgaa gctcttcccc cgctccggg agatgggggc ccgcatgctc	2340
ctccaggctg ccaacgagct cctcctggag gcccccaag cgcgggccga ggagggtggc	2400
gctttggcca aggaggccat ggagaaggcc tatccctcg ccgtgccctt ggagggtggag	2460
gtggggatgg gggaggactg gctttccgcc aagggtcacc accaccacca ccac	2514

<210> 500

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 500

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1 5 10 15
Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20 25 30
Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45
Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60
Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80
Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95
Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
100 105 110
Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125
Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
130 135 140
Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
145 150 155 160
Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser
165 170 175
Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
180 185 190
Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
195 200 205
Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
210 215 220
Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
225 230 235 240
Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
245 250 255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala
 325 330 335
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
 405 410 415
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
 450 455 460
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540
 Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr
 625 630 635 640
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
 645 650 655
 Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 755 760 765
 Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala
 770 775 780
 Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala
 785 790 795 800
 Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro
 805 810 815
 Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
 820 825 830
 His His His His His His
 835

<210> 501

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 501
atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tCGTggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccggc cccacgccc gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc tccccggggt caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgccc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg 900
ccccgcggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020
gcggggctaa aggacctcaa ggaggtcgg ggccctcctcg ccaaggacct cgccgtcttg 1080
gcctcgaggg aggggctaga cctcgtgcc ggggacgacc ccatgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200
gaggacgccc cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
ctcgaggggg aggagaagct cttttggctc taccacgagg tggaaaagcc cctctcccgg 1320
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380
tccttgagc ttgaggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tgetctttga cgagcttagg 1500
cttccgcct tgaagaagac gaagaagaca ggcaagcgt ccaccagcg cgcggtgctg 1560
gaggccctac gggaggccca cccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620
aagctcaaga acacctacgt ggacccccct ccaagcctcg tccacccgag gacgggcgcg 1680
ctccacacc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740
aacctgcaga acatccccgt ccgcaccccc ttgggccaga ggatccgccg ggccttcgtg 1800
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860

gccacacctt ccggggacga aaacctgatc agggctcttc aggaggggaa ggacatccac 1920
 acccagaccg caagctggat gttcggcgtc cccccggagg ccgtggaccc cctgatgcgc 1980
 cgggcgccca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc 2040
 caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100
 ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
 gtggaaaacc tcttcggaag aaggcgctac gtgcccgcacc tcaacgcccg ggtgaagagc 2220
 gtcaggaggc ccgaggagcg catggccttc aacatgcccg tccagggcac cgccgcccac 2280
 ctcatgaagc tcgccatggt gaagctcttc cccgcctcc gggagatggg ggcccgcagc 2340
 ctcctccagg tcgccaacga gtcctcctg gaggcccccc aagcgcgggc cgaggaggcg 2400
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggcg 2460
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 502

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 502

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65				70					75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85					90						95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
	115						120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Gly His His His His His His
835

<210> 503

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 503

atcgtggtct ttgacgccga ggccccctcc ttcc

34

<210> 504

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 504

ggaaggaggg ggccctcggcg tcaaagacca cgat

34

<210> 505

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 505

atgaattcgg aggcgatgct gcccctcttt gagcccaagg gccgggtcct cctggtggac

60

ggccaccacc tggcctaccg caccttcac gccctgaagg gcctcaccac cagccggggg

120

gagccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct caaggaggac

180

ggggacgcgg tgatcgtggt ctttgacgcc gagggcccct ctttcgccca cgaggcctac

240

gggggggtaca aggcggggccg ggccccccacg ccggaggact ttccccggca actcgccttc

300

atcaaggagc	tgggtggacct	cctgggggttc	acgcgcctcg	aggccccggg	ctacgaggcg	360
gacgacgtcc	tggccagcct	ggccaagaag	gcggaaaagg	agggctacga	gtccgcacgc	420
ctcaccgccg	acaaagacct	ttaccagctc	ctttccgacc	gcatccacgt	cctccacccc	480
gaggggtacc	tcatacacc	ggcctggctt	tgggaaaagt	acggcctgag	gcccgaccag	540
tgggccgact	accggggcct	gaccggggac	gagtccgaca	accttcccgg	ggtcaagggc	600
atcggggaga	agacggcgag	gaagcttctg	gaggagtggg	ggagcctgga	agccctcctc	660
aagaacctgg	accggctgaa	gcccgccatc	cgggagaaga	tcctggccca	catggacgat	720
ctgaagctct	cctgggacct	ggccaagggtg	cgcaccgacc	tgcccctgga	ggtggacttc	780
gcaaaaaggc	gggagcccga	ccgggagagg	cttagggcct	ttctggagag	gcttgagttt	840
ggcagcctcc	tccacgagtt	cggccttctg	gaaagcccca	aggccctgga	ggaggccccc	900
tggcccccg	cgggaagggc	cttcgtgggc	tttgtgcttt	cccgaaggga	gcccattgtg	960
gccgatcttc	tggccctggc	cgcgcgcagg	ggcggccgcg	tgcaccgggc	agcagacccc	1020
ttggcggggc	taaaggacct	caaggaggtc	cggggcctcc	tcgccaaggga	cctcgccgtc	1080
ttggcctcga	gggaggggct	agacctcgtg	cccggggacg	accccatgct	cctcgccctac	1140
ctcctggacc	cttcgaacac	cacccccgag	ggggtggcgc	ggcgctacgg	gggggagtg	1200
acggaggacg	cgcgccaccg	ggccctcctc	tcggagaggc	tccatcgga	cctccttaag	1260
cgcctcgagg	gggaggagaa	gctcctttgg	ctctaccacg	aggtggaaaa	gcccctctcc	1320
cgggtcctgg	cccatatgga	ggccaccggg	gtacggcggg	acgtggccta	ccttcaggcc	1380
ctttccctgg	agcttgcgga	ggagatccgc	cgcctcgagg	aggaggtctt	ccgcttgggc	1440
ggccacccct	tcaacctcaa	ctcccgggac	cagctggaaa	gggtgctctt	tgacgagctt	1500
aggcttcccg	ccttgaagaa	gacgaagaag	acaggcaagc	gctccaccag	cgcgcgggtg	1560
ctggaggccc	tacgggaggc	ccacccccatc	gtggagaaga	tcctccagca	ccgggagctc	1620
accaagctca	agaacaccta	cgtggacccc	ctcccaagcc	tcgtccaccc	gaggacgggc	1680
cgcctccaca	cccgttcaa	ccagacggcc	acggccacgg	ggaggcttag	tagctccgac	1740
cccaacctgc	agaacatccc	cgtccgcacc	cccttggggc	agaggatccg	ccgggccttc	1800
gtggccgagg	cgggttgggc	gttgggtggc	ctggactata	gccagataga	gctccgcgtc	1860
ctcgcgccacc	tctccgggga	cgaaaacctg	atcagggtct	tccaggagg	gaaggacatc	1920
cacacccaga	ccgcaagctg	gatgttcggc	gtcccccccg	aggccgtgga	ccccctgatg	1980
cgcggggcgg	ccaagacggt	gaacttcggc	gtcctctacg	gcatgtccgc	ccataggctc	2040
tccaggagc	ttgccatccc	ctacgaggag	gcggtggcct	ttatagagcg	ctacttccaa	2100
agcttcccca	aggtgcgggc	ctggatagaa	aagaccctgg	aggaggggag	gaagcggggc	2160

tacgtggaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc cggggtgaag 2220
 agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc 2280
 gacctcatga agctcgccat ggtgaagctc ttcccccgcc tccgggagat gggggcccgcc 2340
 atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag 2400
 gtggcggtt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag 2460
 gtggaggtgg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac 2520

<210> 506

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 506

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
 1 5 10 15
 Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu
 20 25 30
 Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45
 Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val
 50 55 60
 Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr
 65 70 75 80
 Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
 85 90 95
 Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg
 100 105 110
 Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala
 115 120 125
 Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
 130 135 140
 Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
 145 150 155 160
 Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
 165 170 175
 Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
 180 185 190

Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys
 195 200 205
 Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
 210 215 220
 Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 225 230 235 240
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
 305 310 315 320
 Ala Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830
 Lys Gly His His His His His His
 835 840

<210> 507
 <211> 36
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 507
 cagaccatga attcggaggc gatgctgccc ctcttt 36
 <210> 508
 <211> 36
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 508
 aaagaggggc agcatcgcc cccaattcat ggtctg 36
 <210> 509
 <211> 2517
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 509
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
 caccacctgg cctaccgcac cttctttgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgcagag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgcctcatc 300
 aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccagtcct ccaccccgag 480
 gggtagctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600

ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
aagctctcct	gggacctggc	caaggtgcg	accgacctgc	ccctggaggt	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggccccctgg	900
ccccgcggg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtggggc	960
gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agacccttg	1020
gcggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgcggc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cggcgggacg	tggcctacct	tcaggccctt	1380
tccttgagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
cacccttca	acctcaactc	ccgggaccag	ctggaaaggg	tgtcttttga	cgagcttagg	1500
cttcccgct	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcg	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccccctc	ccaagcctcg	tccacccgag	gacggggccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttgggcccaga	ggatccgccg	ggccttcgtg	1800
gccgaggcgg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gcccacctct	ccggggacga	aaacctgac	agggctttcc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgtc	cccccgagg	ccgtggaccc	cctgatgcgc	1980
cgggcgccca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgccc	taggctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100
ttccccaagg	tgcgggcctg	gatagaaaag	accctggagg	aggggaggaa	gcggggctac	2160
gtggaaaccc	tcttcggaag	aaggcgctac	gtgcccagcc	tcaacgcccg	ggtgaagagc	2220
gtcaggagg	ccgcggagcg	catggccttc	aacatgcccg	tccagggcac	cgccgccgac	2280
ctcatgaagc	tcgccatggt	gaagctcttc	ccccgcctcc	gggagatggg	ggcccgcatg	2340

ctcctccagg tcgccaacga gctcctcctg gagggccccc aagcgcgggc cgaggaggtg 2400
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 510

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 510

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 511
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 511
 gcctaccgca ccttctttgc cctgaagggc etc 33
 <210> 512
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 512
 gagggcccttc agggcaaaga aggtgcggtta ggc 33
 <210> 513
 <211> 2517
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 513
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc ggtcctcct ggtggacggc 60
 caccacctgg cctaccgcac ctccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cgggtctacgg ctccgccaag agcctcctca aggccctcag agaggacggg 180
 gacgcggtga tcgtggtctt tgacgcgag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggcccgggc cccacgccg gaggactttc cccggcaact cgcctcatc 300
 aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
 gggtagctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcac 600

ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
aagctctcct	gggacctggc	caagggtgcg	accgacctgc	ccctggaggt	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggccccctgg	900
cccccgccgg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtggggc	960
gatcttctyg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agacccttg	1020
gcggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgccgc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cggcgggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
cacccttca	acctcaactc	ccgggaccag	ctggaaaagg	tgctctttga	cgagcttagg	1500
cttcccgct	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcgtg	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccccctc	ccaagcctcg	tccacccgag	gacgggcccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttgggccaga	ggatccgccg	ggccttcgtg	1800
gccgaggcgg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gcccacctct	ccggggacga	aaacctgatc	agggctcttc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgtc	cccccgagg	ccgtggaccc	cctgatgcgc	1980
cgggcgggcca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgcccc	taggctctcc	2040
caggagcttg	ccatccccct	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100
ttccccaaag	tgcgggcctg	gatagaaaag	accctggagg	aggggaggaa	gcggggctac	2160
gtggaaaccc	tcttcggaag	aaggcgctac	gtgcccagcc	tcaacgcccg	ggtgaagagc	2220
gtcaggggagg	ccgcggagcg	catggccttc	aacatgcccg	tccagggcac	cgccgccgac	2280
ctcatgaagc	tcgccatggt	gaagctcttc	ccccgcctcc	gggagatggg	ggcccgcatg	2340

ctcctccagg tcgccaacga gctcctcctg gagggccccc aagcgcgggc cgaggaggtg 2400
 gcggcctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 514

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 514

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 515

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 515

ctcctcaagg ccctcagaga ggacggggac gcg

33

<210> 516

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 516

cgcggtccccg tcctctctga gggccttgag gag

33

<210> 517

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 517

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120

ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180

gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggccctacggg 240

gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgccctcatc 300

aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360

gacgtcctgg ccacctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatactc 420

accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480

gggtacctca tcacccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540

gccgactacc gggccctgac cggggacgag tccgacaacc ttcccgggggt caagggcatc 600

ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660

aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggccacat ggacgatctg 720

aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780

aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc	840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg	900
ccccgcggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc	960
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg	1020
gcggggctaa aggacctcaa ggaggtcggg ggccctcctc ccaaggacct cgccgtcttg	1080
gcctcgaggg aggggctaga cctcgtgccc ggggaacgacc ccatgctcct cgcctacctc	1140
ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg	1200
gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc	1260
ctcgagggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg	1320
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt	1380
tccttgagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc	1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg	1500
cttccgcct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg	1560
gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc	1620
aagctcaaga acacctagc ggacccccctc ccaagcctcg tccacccgag gacggggccgc	1680
ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc	1740
aacctgcaga acatccccgt ccgcaccccc ttgggccaga ggatccgccg ggccttcgtg	1800
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc	1860
gcccacctct ccggggacga aaacctgac agggctcttc aggaggggaa ggacatccac	1920
accagaccg caagctggat gttcggcgtc cccccggagg ccgtggaccc cctgatgcgc	1980
cgggcgccca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc	2040
caggagcttg ccatccccctc cgaggaggcg gtggccttta tagagcgcta cttccaaagc	2100
ttccccaagg tgccggcctg gatagaaaag accctggagg aggggaggaa gcggggctac	2160
gtggaaaccc tcttcggaag aaggcgctac gtgcccagacc tcaacgcccg ggtgaagagc	2220
gtcagggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac	2280
ctcatgaagc tcgccatggt gaagctcttc cccgcctcc gggagatggg ggcccgcatg	2340
ctcctccagg tcgccaacga gctcctcctg gagggcccc aagcggggc cgaggagggtg	2400
gcggctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg	2460
gagggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac	2517

<210> 518

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 518

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60
Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
100 105 110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys
115 120 125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
260 265 270
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305 310 315 320
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
325 330 335
Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
340 345 350
Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
355 360 365
Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400
Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
405 410 415
Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
420 425 430
Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
435 440 445
Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
450 455 460
Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
465 470 475 480
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495
Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
500 505 510
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525
Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
530 535 540
Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
545 550 555 560
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 519

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 519
 gacgacgtcc tggccaccct ggccaagaag gcg 33
 <210> 520
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 520
 cgccttcttg gccagggtgg ccaggacgtc gtc 33
 <210> 521
 <211> 2517
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 521
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggctcctct ggtggacggc 60
 caccacctgg cctaccgcac ctccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cgggtctacgg ctccgccaa agcctcctca aggcctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcttacggg 240
 ggggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgcctcatc 300
 aaggagctgg tggacctcct ggggttcacg cgctcgagg tccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tcacgtcct ccaccccgag 480
 gggtagctca tcacccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttccgggggt caagggcatc 600
 ggggagaaga cggcgctcaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggccacat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960

gatcttcttg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agacccttg	1020
gcggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgcggc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cggcgggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaggg	tgctctttga	cgagcttagg	1500
cttccgcct	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcgtg	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccccctc	ccaagcctcg	tccacccgag	gacggggccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttgggccaga	ggatccgccg	ggccttcgtg	1800
gccgaggcgg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gcccacctct	ccggggacga	aaacctgac	agggctcttc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgtc	ccccggagg	ccgtggaccc	cctgatgcgc	1980
cgggcgggcca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgcccc	taggctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100
ttccccaagg	tgcgggcctg	gatagaaaag	accctggagg	aggggaggaa	gcggggctac	2160
gtggaaaccc	tcttcggaag	aaggcgctac	gtgcccagacc	tcaacgcccc	ggtgaagagc	2220
gtcaggagg	ccgcggagcg	catggccttc	aacatgcccc	tccagggcac	cgccgccgac	2280
ctcatgaagc	tcgccatggt	gaagctcttc	ccccgcctcc	gggagatggg	ggcccgcgatg	2340
ctcctccagg	tcgccaacga	gtcctcctcg	gaggcccccc	aagcgggggc	cgaggagggtg	2400
gcggcttttg	ccaaggaggc	catggagaag	gcctatcccc	tcgccgtgcc	cctggagggtg	2460
gaggtgggga	tgggggagga	ctggctttcc	gccaagggtc	accaccacca	ccaccac	2517

<210> 522

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 522

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105						110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150				155						160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165				170						175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
				245					250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 523

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 523

ggggagaaga cggcgctcaa gcttctggag gag

33

<210> 524
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 524
 ctctccaga agcttgagcg ccgtttctc ccc 33
 <210> 525
 <211> 2517
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 525
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cgggtctacgg cttcgccaaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tegtgtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggcccggc cccacgcgc gaggactttc cccggcaact cgccctcatc 300
 aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccagctcct ccaccccag 480
 gggtagctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggaggggctt aaggcctttc tggagaggct tgagtttggc 840
 agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg 900
 ccccgccggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020

gcggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg	1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc	1140
ctggaccctt cgaacaccac ccccaggggg gtggcgcggc gctacggggg ggagtggacg	1200
gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc	1260
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg	1320
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt	1380
tccttgagc ttgcggagga gatccgccg ctcgaggagg aggtcttccg cttggcgggc	1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg	1500
cttcccgcct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg	1560
gaggccctac gggaggccca cccatcgtg gagaagatcc tccagcaccg ggagctcacc	1620
aagctcaaga acacctacgt ggacccccctc ccaagcctcg tccacccgag gacgggccgc	1680
ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc	1740
aacctgcaga acatccccgt ccgcaccccc ttgggccaga ggatccgccg ggcttctgtg	1800
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc	1860
gcccacctct ccggggacga aaacctgac agggctcttc aggaggggaa ggacatccac	1920
accagaccg caagctggat gttcggcgtc cccccggagg ccgtggaccc cctgatgcgc	1980
cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc	2040
caggagcttg ccatccccctc cgaggaggcg gtggccttta tagagcgcta cttccaaagc	2100
ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac	2160
gtggaaaccc tcttcggaag aaggcgctac gtgcccagacc tcaacgcccc ggtgaagagc	2220
gtcagggagg ccgcggagcg catggccttc aacatgcccc tccagggcac cgccgccgac	2280
ctcatgaagc tcgcatggt gaagctcttc cccgcctcc gggagatggg ggcccgcag	2340
ctcctccagg tcgccaacga gtcctcctg gaggcccccc aagcgcgggc cgaggagggtg	2400
gcggctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg	2460
gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac	2517

<210> 526

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 526

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	225	230	235	240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	245	250	255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala	260	265	270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	275	280	285	
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	290	295	300	
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	305	310	315	320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 527

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 527

gagccccgacc gggaggggct taaggccttt ctggagagg

39

<210> 528

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 528
 cctctccaga aaggccttaa gcccctcccc gtcgggctc 39

<210> 529

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 529
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccgggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgcgcag gccccctcct tccgccacga ggcctacggg 240
 ggggtacaagg cgggcccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
 aaggagctgg tggacctcct ggggttcacg cgctcgcagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
 ggggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
 gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
 aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagagggt tgagtttggc 840
 agcctcctcc acgagttcgg ctttctggga ggggagaagc cccgggagga ggccccctgg 900
 cccccgcggg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtggggc 960
 gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agaccccttg 1020
 gcgggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080
 gcctcgcaggg aggggctaga cctcgtgccg ggggacgacc ccatgctcct cgctacctc 1140
 ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200
 gaggacgcgc cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
 ctcgagggggg aggagaagct cttttggctc taccacgagg tggaaaagcc cctctcccgg 1320
 gtcttgcccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380

tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440
 cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500
 cttcccgct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg 1560
 gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620
 aagctcaaga acacctacgt ggacccctc ccaagcctcg tccacccgag gacgggcccgc 1680
 ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740
 aacctgcaga acatccccgt ccgcaccccc ttgggcccaga ggatccgccg ggcttctgtg 1800
 gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860
 gccacacctc ccggggacga aaacctgatc aggtcttcc aggaggggaa ggacatccac 1920
 acccagaccg caagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980
 cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc 2040
 caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100
 ttcccaagg tgccggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
 gtggaaaccc tcttcggaag aaggcgctac gtgcccgaac tcaacgcccg ggtgaagagc 2220
 gtcaggagg cgcgggagcg catggccttc aacatgcccg tccagggcac cgcgcgcgac 2280
 ctcatgaagc tcgcatggt gaagctcttc cccgcctcc gggagatggg ggcccgcgac 2340
 ctctccagg tcgccaacga gtcctcctg gagggccccc aagcgcgggc cgaggaggtg 2400
 gcggctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccaagggtc accaccacca ccaccac 2517

<210> 530

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 530

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 531

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 531
 cacgagttcg gccttctggg aggggagaag ccccgaggagg aggccccctg gcc

54

<210> 532

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 532
 gggccagggg gcctcctccc ggggcttctc ccctcccaga aggccgaact cgtg

54

<210> 533

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 533

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc	60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag	120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgcccag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggcccggc cccacgcgc gaggactttc cccggcaact cgcctcatc	300
aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag	480
gggtacctca tcaccccgcc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg	720
aagctctcct gggacctggc caagggtgcgc accgacctgc cctggagggt ggacttcgcc	780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc	840
agcctcctcc acgagttcgg ccttctggaa agccccaagg cctggaggga ggccccctgg	900
ccccgcgcgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc	960
gatcttctgg ccctggccgc ctgcaggggc ggccgcgtgc accgggcagc agaccccttg	1020
gcggggctaa aggacctcaa ggagggtccgg ggcctcctcg ccaaggacct cgccgtcttg	1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgccctacctc	1140
ctggaccttt cgaacaccac ccccgagggg gtggcgccgc gctacggggg ggagtggacg	1200
gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc	1260
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg	1320
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt	1380
tccttgagc ttgaggagga gatccgcgc ctcgaggagg aggtcttccg cttggcgggc	1440
caccccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg	1500
cttcccgcct tgaagaagac gaagaagaca ggcaagcgt ccaccagcgc cgcggtgctg	1560
gaggccctac gggaggccca cccatcgtg gagaagatcc tccagcaccg ggagctcacc	1620
aagctcaaga acacctacgt ggacccccct ccaagcctcg tccacccgag gacgggcccgc	1680

ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740
aacctgcaga acatccccgt ccgcaccccc ttgggccaga ggatccgccc ggcttcctg 1800
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860
gcccacctct ccggggacga aaacctgatc agggctcttc aggaggggaa ggacatccac 1920
accagaccg caagctggat gttcggcgtc ccccgaggagg ccgtggaccc cctgatgcgc 1980
cgggcgggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc 2040
caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100
ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgcccg ggtgaagagc 2220
gtcaggaggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgcccac 2280
ctcatgaagc tcgccatggt gaagctcttc ccccgccctcc gggagatggg ggcccgcag 2340
ctcctccagg tcgccaacga gctcctcctg gagggccccc aagcgcgggc cgaggagggtg 2400
gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg 2460
gagggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 534

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 534

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
		20						25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50				55					60					
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65				70					75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85					90						95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105						110	

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780

Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830

Gly His His His His His His
 835

<210> 535

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 535
 ctggccctgg ccgcctgcag gggcgccgc gtg

33

<210> 536

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 536
 caccggccg cccctgcagg cggccagggc cag

33

<210> 537

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 537
 atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc

60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag

120

ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg

180

gacgcggtga tcgtggtctt tgacgccgag gccccctcct tcggccacga ggcctacggg

240

gggtacaagg	cgggccgggc	ccccacgccg	gaggactttc	cccggcaact	cgccctcatc	300
aaggagctgg	tggacctcct	ggggttcacg	cgctcgcagg	tcccgggcta	cgaggcggac	360
gacgtcctgg	ccagcctggc	caagaaggcg	gaaaaggagg	gctacgaggt	ccgcatcctc	420
accgccgaca	aagaccttta	ccagctcctt	tccgaccgca	tccacgtcct	ccaccccgag	480
gggtacctca	tcaccccggc	ctggcttttg	gaaaagtacg	gcctgaggcc	cgaccagtgg	540
gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccggggg	caagggcatc	600
ggggagaaga	cggcgaggaa	gcttctgaag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccatat	ggacgatctg	720
aagctctcct	gggacctggc	caaggtgcgc	accgacctgc	ccctggaggt	ggacttcgcc	780
aaaaggcggg	agcccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
agcctcctcc	acgagttcgg	ccttctggaa	agccccaagg	ccctggagga	ggccccctgg	900
ccccgcgcgg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtggggc	960
gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agacccttg	1020
gcggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgcagg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgccgc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggtcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cggcgggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
cacccttca	acctcaactc	ccgggaccag	ctggaaaggg	tgctctttga	cgagcttagg	1500
cttcccgct	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcgtg	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccccctc	ccaagcctcg	tccacccgag	gacgggcccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttgggccaga	ggatccgccg	ggccttcgtg	1800
gccgaggcgg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gccacctct	ccggggacga	aaacctgac	aggtcttcc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgtc	cccccgagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgcca	taggctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100

ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
 gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgcccc ggtgaagagc 2220
 gtcagggagg ccgcggagcg catggccttc aacatgcccc tccagggcac cgccgccgac 2280
 ctcatgaagc tcgccatggt gaagctcttc cccgcctcc gggagatggg ggcccgcagc 2340
 ctctccagg tcgccaacga gctcctcctg gagggccccc aagcgcgggc cgaggaggctg 2400
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggctg 2460
 gaggtgggga tgggggagga ctggctttcc gccaagggtc accaccacca ccaccac 2517

<210> 538

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 538

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75				80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155				160	
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170					175	

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
 355 360 365
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
 405 410 415
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
 420 425 430
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
 450 455 460
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
 530 535 540
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His
 625 630 635 640
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val
 785 790 795 800
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Gly His His His His His His
 835

<210> 539
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 539
 ggggagaaga cggcgaggaa gcttctgaag gagtggggga gc 42
 <210> 540
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 540
 gctccccac tccttcagaa gcttctcgc cgtcttctcc cc 42
 <210> 541
 <211> 2520
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 541
 atgaattcgg aggcgatgct gcccctcttt gagcccaagg gccgggtcct cctggtggac 60
 ggcaccacc tggcctaccg caccttcttt gccctgaagg gcctcaccac cagccggggg 120
 gagccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct cagagaggac 180
 ggggacgcgg tgatcgtggt ctttgacgcc gagggcccct ccttcgcca cgaggcctac 240
 ggggggtaca aggcgggccc ggcacccacg ccggaggact ttccccggca actcgccctc 300
 atcaaggagc tgggtggacct cctgggggttc acgcgcctcg aggtcccggg ctacgaggcg 360
 gacgacgtcc tggccaccct ggccaagaag gcggaaaagg agggctacga ggtccgcata 420
 ctcaccgccg acaaagacct ttaccagctc ctttcgcacc gcatccacgt cctccacccc 480
 gaggggtacc tcatcacccc ggcttggtt tgggaaaagt acggcctgag gcccgaccag 540
 tgggccgact accgggccct gaccggggac gagtccgaca accttcccgg ggtcaagggc 600

atcggggaga agacggcgct caagcttctg gaggagtggg ggagcctgga agccctcctc	660
aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat	720
ctgaagctct cctgggacct ggccaaggtg cgcaccgacc tgcccctgga ggtggacttc	780
gccaaaaggc gggagcccga ccgggagggg cttaaggcct ttctggagag gcttgagttt	840
ggcagcctcc tccacgagtt cggccttctg ggaggggaga agccccggga ggaggcccc	900
tggccccgc cggaaggggc cttcgtgggc tttgtgcttt cccgcaagga gcccatgtgg	960
gccgatcttc tggccctggc cgctgcagg ggcggccgcy tgcaccgggc agcagacccc	1020
ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgccgtc	1080
ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgctac	1140
ctcctggacc cttcgaacac ccccccgag ggggtggcgc ggcgctacgg gggggagtgg	1200
acggaggacg ccgcccaccg ggccctcctc tcggagaggc tccatcgga cctccttaag	1260
cgctcgagg gggaggagaa gctcctttgg ctctaccacg aggtggaaaa gccctctcc	1320
cgggtcctgg cccatatgga ggccaccggg gtacggcggg acgtggccta ccttcaggcc	1380
ctttccctgg agcttgcgga ggagatccgc cgctcgagg aggaggtctt ccgcttggcg	1440
ggccaccct tcaacctcaa ctcccgggac cagctggaaa gggtgctctt tgacgagctt	1500
aggcttcccg ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg	1560
ctggaggccc tacgggaggc ccaccccatc gtggagaaga tcctccagca ccgggagctc	1620
accaagctca agaacacct cgtggacccc ctcccgaagc tcgtccaccc gaggacgggc	1680
cgctccaca ccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac	1740
cccaacctgc agaacatccc cgtccgcacc cccttgggccc agaggatccg ccgggccttc	1800
gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gctccgcgtc	1860
ctcgcccacc tctccgggga cgaaaacctg atcagggtct tcaggagggg gaaggacatc	1920
cacaccaga ccgcaagctg gatgttcggc gtccccccgg aggcctgga cccctgatg	1980
cgccgggcyg ccaagacggt gaacttcggc gtctctacg gcatgtccgc ccataggctc	2040
tccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa	2100
agcttcccca aggtgcgggc ctggatagaa aagacctgg aggaggggag gaagcggggc	2160
tacgtgaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag	2220
agcgtcaggg aggcgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc	2280
gacctcatga agctcgccat ggtgaagctc ttccccgcc tccgggagat gggggccgc	2340

atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag 2400

gtggcggtt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag 2460

gtggaggtgg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac 2520

<210> 542

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 542

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Ala Val
50 55 60

Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr
65 70 75 80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
85 90 95

Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg
100 105 110

Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala
115 120 125

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
130 135 140

Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
145 150 155 160

Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
165 170 175

Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
180 185 190

Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys
195 200 205

Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
210 215 220

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 225 230 235 240
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
 305 310 315 320
 Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830
 Lys Gly His His His His His His
 835 840

<210> 543

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 543

atgaattcgg aggcgatgct gcccctcttt gagcccaagg gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttt gccctgaagg gcctcaccac cagccggggg	120
gagccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct cagagaggac	180
ggggacgcgg tgatcgtggt ctttgacgcc gagggcccct ccttcgccca cgaggcctac	240
ggggggtaca aggcggggcg ggccccacg ccggaggact ttccccggca actcgccctc	300
atcaaggagc tgggtggacct cctgggggttc acgcgcctcg aggtcccggg ctacgaggcg	360
gacgacgtcc tggccaccct ggccaagaag gcggaaaagg agggctacga ggtccgcac	420
ctcaccgcgg acaaagacct ttaccagctc ctttcgcacc gcatccacgt cctccacccc	480
gaggggtacc tcatcaccoc ggccctggctt tgggaaaagt acggcctgag gcccgaccag	540
tgggcccact accggggcct gaccggggac gagtccgaca accttcccgg ggtcaagggc	600
atcggggaga agacggcgct caagcttctg aaggagtggg ggagcctgga agccctcctc	660
aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat	720
ctgaagctct cctgggacct ggccaaggtg cgcaccgacc tgcccctgga ggtggacttc	780
gccaaaaggc gggagcccga ccgggagggg cttaaggcct ttctggagag gcttgagttt	840
ggcagcctcc tccacgagtt cggccttctg ggaggggaga agccccggga ggaggccccc	900
tggccccgc cggaaggggc cttcgtgggc tttgtgcttt cccgcaagga gcccatgtgg	960
gccgatcttc tggccctggc cgcttcgagg ggcgcccgcg tgcaccgggc agcagacccc	1020
ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgcgctc	1080
ttggcctcga gggaggggct agacctcgtg cccggggacg acccatgct cctcgcctac	1140
ctcctggacc cttcgaacac cacccccag ggggtggcgc ggcgctacgg gggggagtgg	1200
acggaggacg ccgcccaccg ggccctcctc tcggagaggc tccatcgga cctccttaag	1260
cgctcagagg gggaggagaa gctcctttgg ctctaccacg aggtggaaaa gccctctcc	1320
cgggtcctgg cccatatgga ggccaccggg gtacggcggg acgtggccta ccttcaggcc	1380
ctttccctgg agcttgcgga ggagatccgc cgctcagagg aggaggtctt ccgcttggcg	1440
ggccaccct tcaacctcaa ctcccgggac cagctggaaa gggtgctctt tgacgagctt	1500
aggcttccc ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg	1560
ctggaggccc tacgggaggc ccaccccatc gtggagaaga tcctccagca ccgggagctc	1620
accaagctca agaacaccta cgtggacccc ctccaagcc tcgtccacc gaggacgggc	1680

cgctccaca cccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac 1740
 cccaacctgc agaacatccc cgtccgcacc cccttggggc agaggatccg ccgggccttc 1800
 gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gctccgcgtc 1860
 ctcgcccacc tctccgggga cgaaaacctg atcagggtct tccaggaggg gaaggacatc 1920
 cacacccaga ccgcaagctg gatgttcggc gtcccccccg aggccgtgga cccctgatg 1980
 cgccgggcg ccaagacggt gaacttcggc gtctctacg gcatgtccgc ccataggctc 2040
 tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa 2100
 agcttcccca aggtgcgggc ctggatagaa aagaccctgg aggaggggag gaagcggggc 2160
 tacgtggaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag 2220
 agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc 2280
 gacctcatga agctcgccat ggtgaagctc ttcccccgcc tccgggagat gggggcccg 2340
 atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag 2400
 gtggcggtt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag 2460
 gtggaggtgg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac 2520

<210> 544

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 544

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Ala	Val
	50					55					60				
Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr
65					70					75				80	
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg
			85						90					95	

Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg
 100 105 110
 Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala
 115 120 125
 Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
 130 135 140
 Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
 145 150 155 160
 Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
 165 170 175
 Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
 180 185 190
 Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys
 195 200 205
 Leu Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
 210 215 220
 Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 225 230 235 240
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
 305 310 315 320
 Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780

Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830

Lys Gly His His His His His His
 835 840

<210> 545

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 545

ggggagaaga cggcgctcag gcttctgaag gagtggggga gcctggaagc

50

<210> 546

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 546

gcttccaggc tccccactc cttcagaagc ttgagcgccg tcttctcccc

50

<210> 547

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 547

ctggtcggga cggacgcaa tgagggtgtg aag

33

<210> 548

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 548

gtccgtccc accagaat

18

<210> 549

<211> 1008

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 549

atgggtgctg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca	60
ggaaagaaaa ttgccgttga tgctttcaac acgtataacc agttcatctc gataataagg	120
cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga	180
atcctataca gagtctccaa catggctcag gtgggaatca ggccggtgtt tgtattcgac	240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag	300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct	360
caggctgcag ggaggggttga cgagtacatt gttgactccg caaagacgct ttttaagttac	420
atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca	480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcgggaagc	540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc	600
tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg	660
acgagggagc agctcatcga catagcgatt ctggtcggga cggacgcaa tgaggggtgtg	720
aaggggtgtc gcgtaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg	780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttctg	840
aatctctctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc	900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttggag	960
aagctcaaag ctctgaagtc aaccaggcc acgcttgaga ggtggttc	1008

<210> 550

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 550

Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
1 5 10 15
Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
20 25 30
Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
35 40 45
Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50 55 60
Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65 70 75 80
Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
85 90 95
Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
100 105 110
Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
115 120 125
Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
130 135 140
Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
145 150 155 160
Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
165 170 175
Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
180 185 190
Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
195 200 205
Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
210 215 220
Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Ala Asn Glu Gly Val
225 230 235 240
Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
245 250 255

tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctggggttg 660
acgaggggagc agctcatcga catagcgatt ctggtcggga cggacaggaa tgaggggtg 720
aaggggtgctg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tatttttcagg 780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg 840
aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc 900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttgagg 960
aagctcaaag ctctgaagtc aaccaggcc acgcttgaga ggtgggttc 1008

<210> 553

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 553

Met	Gly	Ala	Asp	Ile	Gly	Asp	Leu	Phe	Glu	Arg	Glu	Glu	Val	Glu	Leu
1				5					10					15	
Glu	Tyr	Phe	Ser	Gly	Lys	Lys	Ile	Ala	Val	Asp	Ala	Phe	Asn	Thr	Leu
			20					25					30		
Tyr	Gln	Phe	Ile	Ser	Ile	Ile	Arg	Gln	Pro	Asp	Gly	Thr	Pro	Leu	Lys
		35					40					45			
Asp	Ser	Gln	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg
	50					55					60				
Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp
65					70					75					80
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys
				85					90					95	
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly
			100					105					110		
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu
		115					120					125			
Tyr	Ile	Val	Asp	Ser	Ala	Lys	Thr	Leu	Leu	Ser	Tyr	Met	Gly	Ile	Pro
	130					135						140			
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala
145					150					155					160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
 165 170 175
 Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
 195 200 205
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Arg Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335

<210> 554

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 554

gaaccacctc tcaagcgtgg

20

<210> 555

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 555

acgcttgaga ggtggttcct ggaggaggcc ccctgg

36

<210> 556
 <211> 1011
 <212> DNA
 <213> Archaeoglobus fulgidus
 <400> 556
 atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca 60
 ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg 120
 cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga 180
 atcctataca gagtctccaa catggtcgag gtgggaatca ggccgggtgtt tgtattcgac 240
 ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtctgag 300
 gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct 360
 caggctgcag ggaggggttga cgagtacatt gttgactccg caaagacgct ttttaagttac 420
 atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca 480
 gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcgggaagc 540
 ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc 600
 tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctggggttg 660
 acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgagggtgtg 720
 aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg 780
 gcaactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttctg 840
 aatctctctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc 900
 atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttgag 960
 aagctcaaag ctctgaagtc aaccagggcc acgcttgaga ggtgggtctg a 1011
 <210> 557
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 557
 taatctgtat caggctg

17

<210> 558

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 558

```
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgctcttcgt ggtctttgac gccaaagggc cctccttcgg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg tttaccggcc tcgagggtccc cggtacgag 360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgcga cctctaccaa ctctctccg accgcgtcgc cgtcctccac 480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cgggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccaactg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
gagttcggca gcctcctcca cgagttcggc ctctggagg cccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc 960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca 1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttgg cctcgaggga ggggctagac ctctgccccg gggacgaccc catgctcctc 1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgggcg ctacgggggg 1200
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc 1320
ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt 1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttcgcg 1440
ttggcggggc accccttcaa cctcaactcc cgggaccage tggaaagggg gctctttgac 1500
```


gagcttaggc ttcccgctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctcacca agctcaagaa cacctacgtg gacccccctcc caagcctcgt ccacccgagg	1680
acggggccgcc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgacccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgcccg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag	1920
gacatccaca cccagaccgc aagctggatg ttcggcgctc ccccgagggc cgtggacccc	1980
ctgatgcgcc gggcgggccaa gacggtgaac ttcggcgctc tctacggcat gtccgccc	2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100
ttccaaagct tccccaaagt gcgggcctgg atagaaaaga cctggagga ggggaggaag	2160
cggggctacg tggaaacct cttcggaaga aggcgctacg tgcccgacct caacgcccgg	2220
gtgaagagcg tcaggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc	2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg	2340
gcccgcacgc tcctccaggt cgccaacgag ctctcctgg agggccccca agcgcggggc	2400
gaggaggtgg cygctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc	2460
ctggaggtgg aggtggggat gggggaggac tggtttccg ccaagggtca ccaccaccac	2520
caccac	2526

<210> 559

<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 559

atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca	60
ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg	120
cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga	180
atcctataca gagtctccaa catggctcgag gtgggaatca ggccggtggt tgtattcgac	240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag	300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct	360
caggctgcag ggaggggttga cgagtacatt gttgactccg caaagacgct ttttaagttac	420

atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca	480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc	540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc	600
tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg	660
acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgaggggtgtg	720
aaggggtgtc gcgtaagaa ggctttgaac tacatcaaga cctacggaga tatttttcagg	780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttctg	840
aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc	900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttgag	960
aagctcaaag ctctgaagtc aaccaggcc acgcttgaga ggtgggttct ggaggaggcc	1020
ccctggcccc cgccggaagg ggccttcgtg ggcttcgtcc tctcccgccc cgagcccatg	1080
tgggcgagc ttaaagccct ggccgcctgc aggggaggcc gcgtagcaccg ggcagcagac	1140
cccttggcgg ggctaaagga cctcaaggag gtccggggcc tctcgccaa ggacctcgcc	1200
gtcttgccct cgagggaggg gctagacctc gtgcccgggg acgaccccat gctcctcgcc	1260
tacctcctgg acccttcgaa caccaccccc gaggggggtg cgcggcgcta cgggggggag	1320
tggacggagg acgcccacca ccgggcccctc ctctcgga gaagctccatg gaacctcctt	1380
aagcgccctc agggggagga gaagctcctt tggtctacc acgaggtgga aaagcccctc	1440
tcccggtcc tggcccatat ggaggccacc ggggtacggc gggacgtggc ctaccttcag	1500
gccttttccc tggagcttgc ggaggagatc cgccgcctcg agggaggagt cttccgcttg	1560
gcgggcccacc cttcaacct caactcccgg gaccagctgg aaagggtgct ctttgacgag	1620
cttaggcttc ccgccttgaa gaagacgaag aagacaggca agcgctccac cagcgccgcg	1680
gtgctggagg ccctacggga ggcccacccc atcgtagaga agatcctcca gcaccgggag	1740
ctcaccaagc tcaagaacac ctacgtggac cccctcccaa gcctcgtcca cccgaggacg	1800
ggccgcctcc acaccgctt caaccagacg gccacggcca cggggaggct tagtagctcc	1860
gacccaacc tgcagaacat ccccgccgc accccttg ggcagaggat ccgcccggcc	1920
ttcgtggccg aggcgggttg ggcgttggtg gccctggact atagccagat agagctccgc	1980
gtcctcgccc acctctccgg ggacgaaaac ctgatcaggg tcttccagga ggggaaggac	2040
atccacaccc agaccgcaag ctggatgttc ggcgtcccc cggaggccgt ggaccccctg	2100
atgcgcccgg cgccaagac ggtgaacttc ggcgtcctct acggcatgtc cgcccatagg	2160
ctctcccagg agcttgccat cccctacgag gaggcgggtg cctttataga gcgctacttc	2220
caaagcttcc ccaagggtgc ggccctggata gaaaagaccc tggaggaggg gaggaagcgg	2280

ggctacgtgg aaaccctctt cggaagaagg cgctacgtgc cgcacctcaa cgcccgggtg 2340
 aagagcgtca gggaggccgc ggagcgcgatg gccttcaaca tgcccgtcca gggcaccgcc 2400
 gccgacctca tgaagctcgc catggtgaag ctcttcccc gcctccggga gatggggggcc 2460
 cgcagtctcc tccaggctgc caacgagctc ctcttgagg cccccaagc gcggggccgag 2520
 gaggtggcgg ctttggccaa ggaggccatg gagaaggcct atcccctcgc cgtgcccctg 2580
 gaggtggagg tggggatggg ggaggactgg ctttccgcca agggtcacca ccaccaccac 2640
 cac 2643

<210> 560

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 560

Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
 1 5 10 15
 Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
 20 25 30
 Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
 35 40 45
 Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60
 Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
 85 90 95
 Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
 100 105 110
 Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
 115 120 125
 Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
 130 135 140
 Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
 145 150 155 160
 Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
 165 170 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
 195 200 205
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335
 Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
 340 345 350
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala
 355 360 365
 Ala Cys Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly
 370 375 380
 Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala
 385 390 395 400
 Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro
 405 410 415
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
 420 425 430
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg
 435 440 445
 Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu
 450 455 460
 Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu
 465 470 475 480
 Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val
 485 490 495
 Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg
 500 505 510

Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 515 520 525
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro
 530 535 540
 Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 545 550 555 560
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 565 570 575
 Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu
 580 585 590
 Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 595 600 605
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 610 615 620
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 625 630 635 640
 Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln
 645 650 655
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 660 665 670
 Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp
 675 680 685
 Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 690 695 700
 Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 705 710 715 720
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile
 725 730 735
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 740 745 750
 Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly
 755 760 765
 Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg
 770 775 780
 Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 785 790 795 800
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg
 805 810 815
 Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu
 820 825 830
 Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu
 835 840 845

Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
850 855 860

Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His
865 870 875 880

His

<210> 561

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 561
ggttgacttc agagctttga g

21

<210> 562

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 562
aaagctctga agtcaaccct ggaggaggcc ccctgg

36

<210> 563

<211> 2619

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 563
atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca
ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg
cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga
atcctataca gagtctccaa catggtcgag gtgggaatca ggccggtgtt tgtattcgac
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtcgag

60

120

180

240

300

gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct	360
caggctgcag ggaggggtga cgagtacatt gttgactccg caaagacgct ttttaagttac	420
atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca	480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc	540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc	600
tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctggggttg	660
acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgaggggtgtg	720
aaggggtgtcg gcgtaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg	780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg	840
aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc	900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttgag	960
aagctcaaag ctctgaagtc aacctggag gaggccccct ggcccccgcc ggaaggggcc	1020
ttcgtgggct tcgtcctctc ccgccccgag cccatgtggg cggagcttaa agccctggcc	1080
gcctgcaggg gcggccgct gcaccgggca gcagaccct tggcggggct aaaggacctc	1140
aaggagggtcc ggggcctcct cgccaaggac ctgcgcgtct tggcctcgag ggaggggcta	1200
gacctcgtgc ccggggacga ccccatgctc ctgcctacc tcctggacct ttcgaacacc	1260
acccccgagg ggggtggcgcg gcgctacggg ggggagtgga cggaggacgc cgcccaccgg	1320
gccctcctct cggagaggct ccacggaac ctccctaagc gcctcgaggg ggaggagaag	1380
ctcctttggc tctaccacga ggtggaaaag cccctctccc gggctcctggc ccatatggag	1440
gccaccgggg tacggcggga cgtggcctac cttcaggccc tttccctgga gcttgcgag	1500
gagatccgcc gcctcgagga ggaggcttc cgtttggcgg gccaccctt caacctcaac	1560
tcccgggacc agctggaaag ggtgctcttt gacgagctta ggcttcccgc cttgaagaag	1620
acgaagaaga caggcaagcg ctccaccagc gccgcggtgc tggaggccct acgggaggcc	1680
caccccatcg tggagaagat cctccagcac cgggagctca ccaagctcaa gaacacctac	1740
gtggaccccc tccaagcct cgtccacccg aggacgggcc gcctccacac ccgcttcaac	1800
cagacggcca cgccacggg gaggttagt agtccgacc ccaacctgca gaacatcccc	1860
gtccgcaccc ccttgggcca gaggatccgc cgggccttcg tggccgaggc ggggtgggcg	1920
ttggtggccc tggactatag ccagatagag ctccgcgtcc tcgcccacct ctccggggac	1980
gaaaacctga tcagggctct ccaggagggg aaggacatcc acaccagac cgcaagctgg	2040
atgttcggcg tcccccgga ggccgtggac cccctgatgc gccgggcggc caagacggtg	2100
aacttcggcg tcctctacgg catgtccgcc cataggtctt cccaggagct tgccatcccc	2160

tacgaggagg cggtggcctt tatagagcgc tactttccaaa gcttccccaa ggtgcggggcc 2220
 tggatagaaa agaccctgga ggaggggagg aagcggggct acgtggaaac cctcttcgga 2280
 agaaggcgct acgtgcccga cctcaacgcc cggtgaaga gcgtcaggga ggccgcggag 2340
 cgcattggcct tcaacatgcc cgtccagggc accgccgcg acctcatgaa gctcgccatg 2400
 gtgaagctct tccccgcct ccgggagatg ggggcccgc tgcctctcca ggctcgccaac 2460
 gagctcctcc tggaggcccc ccaagcgcgg gccgaggagg tggcggcttt ggccaaggag 2520
 gccatggaga aggcctatcc cctcgccgtg cccctggagg tggaggtggg gatggggggag 2580
 gactggcttt ccgccaaggg tcaccaccac caccaccac 2619

<210> 564

<211> 873

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 564

Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
 1 5 10 15
 Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
 20 25 30
 Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
 35 40 45
 Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60
 Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
 85 90 95
 Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
 100 105 110
 Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
 115 120 125
 Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
 130 135 140
 Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
 145 150 155 160
 Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
 165 170 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
 195 200 205
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320
 Lys Leu Lys Ala Leu Lys Ser Thr Leu Glu Glu Ala Pro Trp Pro Pro
 325 330 335
 Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met
 340 345 350
 Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His
 355 360 365
 Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg
 370 375 380
 Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu
 385 390 395 400
 Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp
 405 410 415
 Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu
 420 425 430
 Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His
 435 440 445
 Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu
 450 455 460
 Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu
 465 470 475 480
 Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu
 485 490 495
 Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu
 500 505 510

Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val
 515 520 525
 Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr
 530 535 540
 Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala
 545 550 555 560
 His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu
 565 570 575
 Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr
 580 585 590
 Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg
 595 600 605
 Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro
 610 615 620
 Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala
 625 630 635 640
 Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His
 645 650 655
 Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp
 660 665 670
 Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala
 675 680 685
 Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val
 690 695 700
 Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro
 705 710 715 720
 Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro
 725 730 735
 Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg
 740 745 750
 Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu
 755 760 765
 Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe
 770 775 780
 Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met
 785 790 795 800
 Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu
 805 810 815
 Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu
 820 825 830
 Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu
 835 840 845

Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser
 850 855 860

Ala Lys Gly His His His His His His
 865 870

<210> 565

<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 565

```

atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtacttctca      60
ggaaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataaagg      120
cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga      180
atcctataca gagtctccaa catggtcgag gtgggaatca ggccggtgtt tgtattcgac      240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggctgag      300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct      360
caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct ttttaagttac      420
atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca      480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc      540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc      600
tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg      660
acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgaggggtgtg      720
aagggtgtcg gcgtaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg      780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttctg      840
aatcctctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc      900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttgag      960
aagctcaaag ctctgaagtc aaccaggcc acgcttgaga ggtggttcct ggaggaggcc      1020
ccctggcccc cgccggaagg ggccttcgtg ggcttcgtcc tctccgccc cgagcccatg      1080
tgggcggagc ttaaagccct ggccgctgc aggggcggcc gcgtccaccg ggcccccgag      1140
ccttataaag cctcaggga cctgaaggag gcgcgggggc ttctcgcaa agacctgagc      1200
gttctggccc tgagggaagg ccttggcctc ccgcccggcg acgaccccat gctcctcgcc      1260
tacctcctgg acccttcgaa caccaccccc gagggggtgg cccggcgcta cggcggggag      1320

```

tggacggagg	aggcggggga	gcggggccgcc	ctttccgaga	ggctcttcgc	caacctgctt	1380
aagaggcttg	agggggagga	gaggctcctt	tggctttacc	gggaggtgga	gaggccccctt	1440
tccgctgtcc	tggcccatat	ggaggccacg	ggggtgcgcc	tggacgtggc	ctatctcagg	1500
gccttgtccc	tggaggtggc	cgaggagatc	gcccgcctcg	aggccgaggt	cttccgcctg	1560
gccggccacc	ccttcaacct	caactcccgg	gaccagctgg	aaagggtcct	ctttgacgag	1620
ctagggttcc	ccgccatcaa	gaagacgcaa	aagaccggca	agcgctccac	cagcgccgcc	1680
gtcctggagg	ccctccgcga	ggcccccccc	atcgtggaga	agatcctgca	gtaccgggag	1740
ctcaccaagc	tgaagagcac	ctacattgac	cccttgccgg	acctcatcca	ccccaggacg	1800
ggcgcgcctcc	acacccgctt	caaccagacg	gccacggcca	cgggcagggt	aagtagctcc	1860
gatcccaacc	tccagaacat	ccccgtccgc	accccgcttg	ggcagaggat	ccgccggggcc	1920
ttcatcgccg	aggaggggtg	gctattggtg	gccctggact	atagccagat	agagctcagg	1980
gtgctggccc	acctctccgg	cgacgagaa	ctgatccggg	tcttccagga	ggggcgggac	2040
atccacacgg	agaccgccag	ctggatgttc	ggcgcccccc	gggaggccgt	ggacccccctg	2100
atgcgccggg	cggccaagac	catcaacttc	ggggtcctct	acggcatgtc	ggccccaccgc	2160
ctctcccagg	agctagccat	cccttacgag	gaggcccagg	ccttcattga	gcgctacttt	2220
cagagcttcc	ccaaggtgcg	ggcctggatt	gagaagaccc	tggaggaggg	caggaggcgg	2280
gggtacgtgg	agaccctctt	cgcccgccgc	cgctacgtgc	cagacctaga	ggccccgggtg	2340
aagagcgtgc	gggaggcggc	cgagcgcgatg	gccttcaaca	tgcccgtcca	gggcaccgcc	2400
gccgacctca	tgaagctggc	tatggtgaag	ctcttcccca	ggctggagga	aatggggggcc	2460
aggatgctcc	ttcaggtcgc	caacgagctg	gtcctcgagg	ccccaaaaga	gagggcggag	2520
gccgtggccc	ggctggccaa	ggaggatcatg	gagggggtgt	atcccctggc	cgtgccccctg	2580
gaggtggagg	tggggatagg	ggaggactgg	ctctccgcca	aggagcacca	ccaccaccac	2640
cac						2643

<210> 566

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 566

Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
1 5 10 15
Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
20 25 30
Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
35 40 45
Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50 55 60
Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65 70 75 80
Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
85 90 95
Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
100 105 110
Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
115 120 125
Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
130 135 140
Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
145 150 155 160
Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
165 170 175
Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
180 185 190
Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
195 200 205
Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
210 215 220
Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
225 230 235 240
Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
245 250 255
Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
260 265 270
Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
275 280 285
Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
290 295 300
Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
305 310 315 320

Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335
 Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
 340 345 350
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala
 355 360 365
 Ala Cys Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
 370 375 380
 Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
 385 390 395 400
 Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
 405 410 415
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
 420 425 430
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
 435 440 445
 Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Leu Lys Arg Leu Glu
 450 455 460
 Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu
 465 470 475 480
 Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
 485 490 495
 Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg
 500 505 510
 Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 515 520 525
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro
 530 535 540
 Ala Ile Lys Lys Thr Gln Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 545 550 555 560
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 565 570 575
 Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu
 580 585 590
 Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 595 600 605
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 610 615 620
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 625 630 635 640
 Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln
 645 650 655

Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile
			660					665					670		
Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Glu	Thr	Ala	Ser	Trp
			675				680					685			
Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala
			690				695				700				
Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg
705					710					715					720
Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Gln	Ala	Phe	Ile
				725					730					735	
Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys
			740					745					750		
Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly
		755					760					765			
Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg	Val	Lys	Ser	Val	Arg
			770			775					780				
Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala
785					790					795					800
Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Glu
				805					810					815	
Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	Ala	Asn	Glu	Leu	Val	Leu
			820					825					830		
Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala	Arg	Leu	Ala	Lys	Glu
			835				840					845			
Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val
			850			855					860				
Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu	His	His	His	His	His
865					870					875					880

His

<210> 567

<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 567

atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca	60
ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg	120
cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga	180
atcctataca gagtctccaa catggtcgag gtgggaatca ggccggtgtt tgtattcgac	240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtctgag	300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct	360
caggctgcag ggaggggttga cgagtacatt gttgactccg caaagacgct ttttaagttac	420
atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca	480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaaagc	540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttccccg caaaaatgtc	600
tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg	660
acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgaggggtgtg	720
aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tatttttcagg	780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg	840
aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc	900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggcccttgag	960
aagctcaaag ctctgaagtc aaccagggcc acgcttgaga ggtgggttcc ggaggaggcc	1020
ccctggcccc cgccggaagg ggcccttcgtg ggcttcgtcc tctcccgccc cgagcccatg	1080
tgggcggagc ttaaagccct ggccgcctgc aggggcggcc gcgtccaccg ggcccccgag	1140
ccttataaag ccctcagggc cctgaaggag gcgcgggggc ttctcgccaa agacctgagc	1200
gttctggccc tgaggggaagg ccttggcctc ccgcccggcg acgaccccat gctcctcgcc	1260
tacctcctgg acccttcgaa caccaccccc gaggggggtgg cccggcgcta cggcggggag	1320
tggacggagg aggcggggga gcgggcccgc ctttccgaga ggctcttcgc caacctgtgg	1380
gggaggcttg agggggagga gaggtcctt tggttttacc gggagggtga gagggccctt	1440
tccgctgtcc tggcccatat ggaggccacg ggggtgcgcc tggacgtggc ctatctcagg	1500
gccttgtccc tggaggtggc cgaggagatc gccgcctcg aggcgaggt cttccgcctg	1560
gccggccacc ccttcaacct caactcccgg gaccagctgg aaagggtcct ctttgacgag	1620
ctagggttcc ccgccatcgg caagacggag aagaccggca agcgctccac cagcgccgcc	1680
gtcctggagg ccctccgcga ggcccacccc atcgtggaga agatcctgca gtaccgggag	1740
ctaccaagc tgaagagcac ctacattgac cccttgccgg acctcatcca ccccaggacg	1800
ggccgcctcc acaccgctt caaccagacg gccacggcca cgggcaggct aagtagctcc	1860

gatcccaacc tccagaacat ccccgctccgc accccgcttg ggagaggat ccgcccgggcc 1920
 ttcacgcgcg aggggggtg gctattggtg gccctggact atagccagat agagctcagg 1980
 gtgctggccc acctctccgg cgacgagaac ctgatccggg tcttcaggga ggggcccggac 2040
 atccacacgg agaccgccag ctggatgttc ggcgcccccc gggaggccgt ggaccccctg 2100
 atgcgcgcgg cgccaagac catcaacttc ggggtcctct acggcatgtc ggcccaccgc 2160
 ctctcccagg agctagccat cccttacgag gaggcccagg ccttcattga gcgctacttt 2220
 cagagcttcc ccaagggtgcg ggcttggtt gagaagaccc tggaggaggg caggaggcgg 2280
 ggggtacgtg agaccctctt cggccgcgcg cgctacgtgc cagacctaga ggcccgggtg 2340
 aagagcgtgc gggaggcggc cgagcgcgtg gccttcaaca tgcccgtcca gggcaccgcc 2400
 gccgacctca tgaagctggc tatggtgaag ctcttcccca ggctggaggga aatggggggcc 2460
 aggatgctcc ttcagggtcca caacgagctg gtcctcgagg ccccaaaaga gagggcggag 2520
 gccgtggccc ggctggccaa ggaggtcatg gaggggggtg atcccctggc cgtgcccctg 2580
 gaggtggagg tggggatagg ggaggactgg ctctccgcca aggagcacca ccaccaccac 2640
 cac 2643

<210> 568

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 568

Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
 1 5 10 15
 Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
 20 25 30
 Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
 35 40 45
 Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60
 Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
 85 90 95
 Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
 100 105 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
 115 120 125
 Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
 130 135 140
 Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
 145 150 155 160
 Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
 165 170 175
 Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
 195 200 205
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335
 Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
 340 345 350
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala
 355 360 365
 Ala Cys Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
 370 375 380
 Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
 385 390 395 400
 Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
 405 410 415
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
 420 425 430
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
 435 440 445

Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu
 450 455 460
 Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu
 465 470 475 480
 Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
 485 490 495
 Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg
 500 505 510
 Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 515 520 525
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro
 530 535 540
 Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 545 550 555 560
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 565 570 575
 Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu
 580 585 590
 Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 595 600 605
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 610 615 620
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 625 630 635 640
 Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln
 645 650 655
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 660 665 670
 Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp
 675 680 685
 Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 690 695 700
 Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 705 710 715 720
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile
 725 730 735
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 740 745 750
 Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly
 755 760 765
 Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg
 770 775 780

Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 785 790 795 800
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu
 805 810 815
 Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asn Glu Leu Val Leu
 820 825 830
 Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu
 835 840 845
 Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
 850 855 860
 Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu His His His His His
 865 870 875 880

His

<210> 569

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 569

gagcggataa caatttcaca cagg

24

<210> 570

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 570

tgccccggtgc acgcgggcgc ccctgcaggc

30

<210> 571

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 571

atgaattccc tgccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac	60
ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc	120
caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tgtttgacgc caaggccccc tccttcgcgc accagacctt cgaggcctac	240
aaggcggggc gggctccccc ccccgaggac tttccccggc agcttgccct tatcaaggag	300
atggtggacc ttttgggcct ggagcgctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggccgaaaag gagggctacg aggtccgcat cctcaccgcc	420
gacaaagacc tttaccagct cctttccgac cgcattccacg tcctccaccc cgaggggtac	480
ctcatcaccc cggcctggct ttgggâaaag tacggcctga ggcccgacca gtgggcccgc	540
taccgggccc tgaccgggga cgagtcgcgc aaccttcccg gggtaaggc catcggggag	600
aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg	660
gaccggctga agcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc	720
tcctgggacc tggccaaggt gcgcacgcgc ctgcccctgg aggtggactt cgccaaaagg	780
cgggagcccc accgggaggg ggagaagccc cgggaggagg cccctggcc cccgcccga	840
ggggccttcg tgggcttcct cctttccgc cccgagccca tgtgggcgga gcttaaagcc	900
ctggccgctt gcaggggcgg ccgcgtgcac cgggcagcag accccttggc ggggctaaag	960
gacctcaagg aggtccgggg cctcctcgcc aaggacctcg ccgtcttggc ctcgaggag	1020
gggctagacc tcgtgcccgg ggacgacccc atgtcctcg cctacctctt ggaccttcg	1080
aacaccaccc ccgagggggg ggcgcggcgc tacggggggg agtggacgga ggacgcgc	1140
caccgggccc tcctctcgga gaggtccat cggaacctcc ttaagcgctt cgagggggag	1200
gagaagctcc tttggctcta ccacgaggtg gaaaagcccc tctccgggt cctggcccat	1260
atggaggcca ccggggtacg gcgggacgtg gcctaccttc aggcctttc cctggagctt	1320
gcggaggaga tccgcgcct cgaggaggag gtcttcgcgt tggcgggcca ccccttcaac	1380
ctcaactccc gggaccagct ggaaaggggt ctctttgacg agcttaggtt tccgccttg	1440
aagaagacga agaagacagg caagcgctcc accagcgccg cgggtgctgga ggccctacg	1500
gaggcccacc ccatcgtgga gaagatcctc cagcaccggg agctcaccaa gctcaagaac	1560
acctacgtgg acccctccc aagcctcgtc caccgagga cgggcgcct ccacaccgc	1620
ttcaaccaga cggccacggc cacggggagg cttagtagct ccgaccccaa cctgcagaac	1680
atccccgtcc gcacccctt gggccagagg atccgcggg ccttcgtggc cgaggcgggt	1740
tgggcgttgg tggccctgga ctatagccag atagagctcc gcgtcctcgc ccacctctcc	1800
ggggacgaaa acctgatcag ggtcttcag gaggggaagg acatccacac ccagaccgca	1860

agctggatgt tcggcgctccc cccggaggcc gtggaccccc tgatgcgccg ggcgggccaag 1920
 acggtgaact tcggcgctcct ctacggcatg tccgcccata ggctctccca ggagcttgcc 1980
 atccccctacg aggaggcggt ggcctttata gagcgctact tccaaagctt cccaaggtg 2040
 cgggcctgga tagaaaagac cctggaggag gggaggaagc ggggctacgt ggaaaccctc 2100
 ttcggaagaa ggcgctacgt gcccgcctc aacgcccggg tgaagagcgt cagggaggcc 2160
 gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgcccacct catgaagctc 2220
 gccatggtga agctcttccc ccgcctccgg gagatggggg ccgcatgct cctccaggtc 2280
 gccaacgagc tcctcctgga ggccccccaa gcgcgggccg aggaggtggc ggctttggcc 2340
 aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtggggatg 2400
 ggggaggact ggctttccgc caagggtcac caccaccacc accac 2445

<210> 572

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 572

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	1	5	10	15
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu	20	25	30	
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	Asp	Leu	130	135	140	

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
 145 150 155 160
 Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
 165 170 175
 Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
 180 185 190
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
 195 200 205
 Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
 210 215 220
 Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
 225 230 235 240
 Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255
 Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
 260 265 270
 Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
 275 280 285
 Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
 290 295 300
 Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
 305 310 315 320
 Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
 325 330 335
 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
 340 345 350
 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365
 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380
 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
 420 425 430
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445
 Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480

Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
 530 535 540
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
 545 550 555 560
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 645 650 655
 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
 660 665 670
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 675 680 685
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 690 695 700
 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
 705 710 715 720
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
 725 730 735
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
 740 745 750
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
 755 760 765
 Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
 770 775 780
 Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
 785 790 795 800
 Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
 805 810 815

<210> 573
 <211> 2520
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 573
 atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct caaggaggac 180
 ggggacgcgg tgatcgtggt ctttgacgcc aaggccccct ccttcgccca cgaggcctac 240
 ggggggtaca aggcggggcg gggccccacc ccggaggact tccccgccca gctcgccttg 300
 gtcaagcggc tgggtggacct tctgggcctg gtccgcctcg agggcccggg gtacgaggcg 360
 gacgacgtcc tgggcaccct ggccaagaag gccgaaaagg aggggtacga ggtgcgcac 420
 ctcaccgccg accgcgacct ctaccaactc gtctccgacc gcattccacgt cctccacccc 480
 gaggggtacc tcatcacccc ggagtggctt tgggagaagt atgggcttaa gccttcccag 540
 tgggtggact accgggcctt ggccggggac ccttcgcaca acatccccgg cgtgaagggc 600
 atcggggaga agacggcggc caagctgac cgggagtggt gaagcctgga aaacctcctc 660
 aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat 720
 ctgaagctct cctgggacct ggccaagggt cgcaccgacc tgccccgga ggtggacttc 780
 gccaaaaggc gggagccccg ccgggagagg cttagggcct ttctggagag gcttgagttt 840
 ggcagcctcc tccacgagtt cggccttctg gaaagcccca aggccttggg ggaggccccc 900
 tggccccgc cggaaggggc cttcgtgggc ttcgtcctct cccgccccga gcccatgtgg 960
 gcggagctta aagccctggc cgcctgcagg ggcggccgcg tgcaccgggc agcagacccc 1020
 ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgcgcgc 1080
 ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgcctac 1140
 ctctggacc cttcgaacac ccccccgag ggggtggcgc ggcgctacgg gggggagtgg 1200
 acggaggacg ccgcccaccg ggccctcctc tcggagaggc tccatcgga cctccttaag 1260
 cgcctcgagg gggaggagaa gtccttttgg ctctaccacg aggtggaaaa gccctctcc 1320
 cgggtcctgg cccatatgga ggccaccggg gtacggcggg acgtggccta ccttcaggcc 1380
 ctttccttgg agcttgcgga ggagatccgc cgcctcgagg aggaggtctt ccgcttggcg 1440
 ggccaccctc tcaacctcaa ctcccgggac cagctggaaa ggggtgctct tgacgagctt 1500

aggcttcccc ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg 1560
 ctggaggccc tacgggaggg ccaccccatc gtggagaaga tcctccagca ccgggagctc 1620
 accaagctca agaacaccta cgtggacccc ctcccaagcc tcgtccaccc gaggacgggc 1680
 cgcctccaca cccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac 1740
 cccaacctgc agaacatccc cgtccgcacc cccttggggc agaggatccg ccgggccttc 1800
 gtggccgagg cggttgggc gttggtggcc ctggactata gccagataga gctccgcgtc 1860
 ctgccccacc tctccgggga cgaaaacctg atcagggtct tccaggaggg gaaggacatc 1920
 cacaccaga ccgcaagctg gatgttcggc gtccccccgg aggccgtgga cccctgatg 1980
 cgccggggcg ccaagacggt gaacttcggc gtccctctacg gcatgtccgc ccataggctc 2040
 tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa 2100
 agcttcccca aggtgcgggc ctggatagaa aagaccctgg aggaggggag gaagcggggc 2160
 tacgtggaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag 2220
 agcgtcaggg aggcgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc 2280
 gacctcatga agctcgccat ggtgaagctc ttccccgcc tccgggagat gggggcccg 2340
 atgtctctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag 2400
 gtggcggctt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag 2460
 gtggaggtgg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac 2520

<210> 574

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 574

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val
	50					55				60					
Ile	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr
65					70					75				80	

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
 85 90 95
 Gln Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg
 100 105 110
 Leu Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala
 115 120 125
 Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
 130 135 140
 Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Ile His Val Leu His Pro
 145 150 155 160
 Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu
 165 170 175
 Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser
 180 185 190
 Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys
 195 200 205
 Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp
 210 215 220
 Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 225 230 235 240
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
 305 310 315 320
 Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
770 775 780

Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
785 790 795 800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
805 810 815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
820 825 830

Lys Gly His His His His His His
835 840

<210> 575

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 575

atgaattccc tgccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac	60
ctggcctacc gtacctttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc	120
caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tgtttgacgc caaggcccc tccttccgcc accagaccta cgaggcctac	240
aaggcggggc gggctccac ccccgaggac tttccccggc agcttgccct tatcaaggag	300
atggtggacc ttttgggctt taccgcctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaaaag gagggctacg aggtccgcat cctcaccgcc	420
gacaaagacc tttaccagct cctttccgac cgcattccacg tcctccaccc cgaggggtac	480
ctcatcacc cggcctggct ttgggaaaag tacggcctga ggcccgaaca gtgggccgac	540
taccgggccc tgaccgggga cgagtccgac aaccttcccg gggccaagg catcggggag	600
aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg	660
gaccggctga agcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc	720
tcctgggacc tggccaaggt gcgcaccgac ctgcccctgg aggtggactt cgccaaaagg	780
cgggagcccc accgggaggg ggagaagccc cgggaggagg cccctggcc cccgcccga	840
ggggccttcg tgggcttct cctttccgc cccgagccca tgtgggcgga gcttaaagcc	900
ctggccgcct gcaggggcgg ccgcgtgcac cgggcagcag accccttggc ggggctaaag	960

gacctcaagg aggtccgggg cctcctcgcc aaggacctcg ccgtcttggc ctcgagggag	1020
gggctagacc tcgtgcccgg ggacgacccc atgctcctcg cctacctcct ggacccttcg	1080
aacaccacccc ccgaggggggt ggcgcggcgc tacggggggg agtggacgga ggacgccgccc	1140
caccggggccc tcctctcgga gaggtccat cggaacctcc ttaagcgct cgagggggag	1200
gagaagctcc tttggctcta ccacgaggtg gaaaagcccc tctcccggt cctggcccat	1260
atggaggcca cgggggtacg gcgggacgtg gcctaccttc aggccttttc cctggagctt	1320
gcggaggaga tccgccgcct cgaggaggag gtcttcgcgt tggcgggcca ccccttcaac	1380
ctcaactccc gggaccagct ggaaaggggt ctctttgacg agcttaggct tccgccttg	1440
aagaagacga agaagacagg caagcgctcc accagcgccg cggtgctgga ggccctacgg	1500
gaggccccacc ccatcggtga gaagatcctc cagcaccggg agctcaccaa gctcaagaac	1560
acctacgtgg accccctccc aagcctcgtc caccgagga cgggccgcct ccacaccgc	1620
ttcaaccaga cgccacggc cacggggagg cttagtagct ccgaccccaa cctgcagaac	1680
atccccgtcc gcacccctt gggccagagg atccgcggg ccttcgtggc cgaggcgggt	1740
tgggcgttg tggccctgga ctatagccag atagagctcc gcgtcctgc ccacctctcc	1800
ggggacgaaa acctgatcag ggtcttcag gaggggaagg acatccacac ccagaccgca	1860
agctggatgt tcggcgctcc cccggaggcc gtggaccccc tgatgcgcgc ggcggccaag	1920
acggtgaact tcggcgctct ctacggcatg tccgccata ggctctccca ggagcttgcc	1980
atcccctacg aggaggcggg ggcctttata gagcgctact tccaaagctt ccccaagggtg	2040
cgggcctgga tagaaaagac cctggaggag gggaggaagc ggggctacgt ggaaaccctc	2100
ttcgaagaa ggcgctacgt gcccgacctc aacgcccggg tgaagagcgt caggagggcc	2160
gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc	2220
gccatggtga agctcttccc ccgcctccgg gagatggggg cccgcatgct cctccaggtc	2280
gccaacgagc tcctcctgga ggccccccaa gcgcgggccg aggaggtggc ggctttggcc	2340
aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtggggatg	2400
ggggaggact ggctttccgc caagggtcac caccaccacc accac	2445

<210> 576

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 576

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	1	5	10	15
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu	20	25	30	
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	Asp	Leu	130	135	140	
Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly	Tyr	145	150	155	160
Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Asp	165	170	175	
Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn	Leu	180	185	190	
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	Glu	195	200	205	
Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	Lys	210	215	220	
Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys	Leu	225	230	235	240
Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp	245	250	255	
Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Glu	Lys	Pro	Arg	Glu	260	265	270	
Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Leu	Leu	275	280	285	
Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	290	295	300	
Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	305	310	315	320

Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
 325 330 335
 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
 340 345 350
 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365
 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380
 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
 420 425 430
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445
 Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480
 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
 530 535 540
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
 545 550 555 560
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 645 650 655

Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
 660 665 670
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 675 680 685
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 690 695 700
 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
 705 710 715 720
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
 725 730 735
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
 740 745 750
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Glu Ala
 755 760 765
 Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
 770 775 780
 Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
 785 790 795 800
 Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
 805 810 815

<210> 577

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 577

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct caaggaggac 180
 ggggacgcgg tgategtggt ctttgacgcc aaggccccct ctttcgccca cgaggcctac 240
 ggggggtaca aggcggggccg ggccccccacc ccggaggact tcccccgcca gctcgccttg 300
 gtcaagcggc tgggtggacct tctgggcttt accgcctcg agggccccgg gtacgaggcg 360
 gacgacgtcc tgggcaccct ggccaagaag gccgaaaagg aggggtacga ggtgcgcac 420
 ctcaccgccg accgcgacct ctaccaactc gtctccgacc gcatccacgt cctccacccc 480
 gaggggtacc tcatcacccc ggagtggctt tgggagaagt atgggcttaa gccttcccag 540
 tgggtggact accgggcctt ggccggggac ctttcgcaca acatccccgg cgtgaagggc 600

atcggggaga agacggcggc caagctgata cgggagtggg gaagcctgga aaacctcctc	660
aagaacctgg accggtgaa gcccgccatc cgggagaaga tcctggccca catggacgat	720
ctgaagctct cctgggacct ggccaagggtg cgcaccgacc tgcccctgga ggtggacttc	780
gccaaaaggc gggagccccga ccgggagagg cttagggcct ttctggagag gcttgagttt	840
ggcagcctcc tccacgagtt cggccttctg gaaagcccca aggccctgga ggaggccccc	900
tggccccgc cggaaggggc cttcgtgggc ttcgtcctct cccgccccga gcccatgtgg	960
gcggagctta aagccctggc cgcctgcagg ggcggccgcg tgcaccgggc agcagacccc	1020
ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaaagga cctcgccgtc	1080
ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgccctac	1140
ctcctggacc cttcgaacac ccccccgag ggggtggcgc ggcgctacgg gggggagtgg	1200
acggaggacg ccgcccaccg ggccctcctc tcggagaggc tccatcgga cctccttaag	1260
cgctcgagg gggaggagaa gctcctttgg ctctaccacg aggtggaaaa gccctctcc	1320
cgggtcctgg cccatatgga ggccaccggg gtacggcggg acgtggccta ccttcaggcc	1380
ctttccctgg agcttgcgga ggagatccgc cgcctcgagg aggaggtctt ccgcttggcg	1440
ggccaccct tcaacctcaa ctcccgggac cagctggaaa ggggtgctctt tgacgagctt	1500
aggcttcccg ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg	1560
ctggaggccc tacgggaggc ccaccccatc gtggagaaga tcctccagca ccgggagctc	1620
accaagctca agaacacct cgtggacccc ctcccaagcc tcgtccacc gaggaagggc	1680
cgctccaca ccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac	1740
cccaacctgc agaacatccc cgtccgcacc cccttgggccc agaggatccg ccgggccttc	1800
gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gctccgcgtc	1860
ctcgcccacc tctccgggga cgaaaacctg atcagggtct tccaggaggg gaaggacatc	1920
cacaccacaga ccgcaagctg gatgttcggc gtccccccgg aggccgtgga cccctgatg	1980
cgcggggcgg ccaagacggt gaacttcggc gtctctacg gcatgtccgc ccataggctc	2040
tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa	2100
agcttcccca aggtgcgggc ctggatagaa aagaccctgg aggaggggag gaagcggggc	2160
tacgtggaaa cctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag	2220
agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgcgcgc	2280
gacctcatga agctcgccat ggtgaagctc ttcccccgcc tccgggagat gggggccgcg	2340

atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag 2400
 gtggcgggctt tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag 2460
 gtggagggtgg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac 2520

<210> 578

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 578

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	50	55	60	
Ile	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	65	70	75	80
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	85	90	95	
Gln	Leu	Ala	Leu	Val	Lys	Arg	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	100	105	110	
Leu	Glu	Ala	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Gly	Thr	Leu	Ala	115	120	125	
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	130	135	140	
Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	145	150	155	160
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	165	170	175	
Lys	Pro	Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	180	185	190	
Asp	Asn	Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	195	200	205	
Leu	Ile	Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	210	215	220	

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 225 230 235 240
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
 305 310 315 320
 Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830
 Lys Gly His His His His His His
 835 840

<210> 579

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 579

atgaattccc tgccctcttt tgagcccaag ggccgggtgc ttctggtgga cggccaccac	60
ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc	120
caggcggtgt acgggttttg caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tctttgacgc cgaggccccc tccttccgcc accagaccta cgaggcctac	240
aaggcggggc gggctcccac ccccgaggac tttccccggc agcttgccct tatcaaggag	300
atggtggacc ttttgggcct ggagcgcctc gagtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaagaa gagggctacg aggtccgcat cctcaccgcc	420
gacaaagacc ttaccagct cttttccgac cgcattccacg tctccacccc cgaggggtac	480
ctcatcaccc cggcctggct ttgggaaaag tacggcctga ggcccgacca gtgggcccgc	540
taccgggccc tgaccgggga cgagtccgac aaccttcccg gggtaaggag catcggggag	600
aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg	660
gaccggctga agcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc	720
tcctgggacc tggccaaggt gcgcaccgac ctgcccctgg aggtggactt cgccaaaagg	780
cgggagcccg accgggaggg ggagaagccc cgggaggagg cccctggcc cccgcccga	840
ggggccttcg tgggcttct cttttccgc cccgagccca tgtgggcgga gcttaaagcc	900
ctggccgcct gcaggggcgg ccgcgtgcac cgggcagcag accccttggc ggggctaaag	960
gacctcaagg aggtccgggg cctcctcgcc aaggacctcg ccgtcttggc ctcgaggag	1020
gggctagacc tcgtgcccgg ggacgacccc atgctcctcg cctacctct ggaccttcg	1080
aacaccaccc ccgagggggg ggcgcggcgc tacggggggg agtggacgga ggacgccgcc	1140
caccgggccc tcctctcgga gaggtccat cggaacctcc ttaagcgctt cgagggggag	1200
gagaagctcc tttggctcta ccacgaggtg gaaaagcccc tctccgggt cctggcccat	1260
atggaggcca ccggggtacg gcgggacgtg gctaccttc aggcctttc cctggagctt	1320
gcggaggaga tccgcgcct cgaggaggag gtcttccgct tggcgggcca ccccttcaac	1380
ctcaactccc gggaccagct ggaaagggtg ctctttgacg agcttaggt tccgccttg	1440
aagaagacga agaagacagg caagcgtcc accagcgccg cggtgctgga ggccctacgg	1500
gaggcccacc ccatcgtgga gaagatctc cagcaccggg agctcaccaa gctcaagaac	1560
acctacgtgg accccctccc aagcctcgtc caccgagga cgggcgcct ccacaccgc	1620
ttcaaccaga cggccacggc cagggggagg cttagtagct ccgaccccaa cctgcagaac	1680

atccccgtcc gcaccccctt gggccagagg atccgccggg ccttcgtggc cgaggcgggt 1740
 tgggcgttgg tggccctgga ctatagccag atagagctcc gcgtcctcgc ccacctctcc 1800
 ggggacgaaa acctgatcag ggtcttccag gaggggaagg acatccacac ccagaccgca 1860
 agctggatgt tcggcgctcc cccggaggcc gtggaccccc tgatgcgccg ggcggccaag 1920
 acggtgaact tcggcgctct ctacggcatg tccgcccata ggctctccca ggagcttgcc 1980
 atccccctacg aggaggcggg ggcctttata gagcgctact tccaaagctt cccaaggtg 2040
 cgggcctgga tagaaaagac cctggaggag gggaggaagc ggggctacgt ggaaaccctc 2100
 ttcggaagaa ggcgctacgt gcccgcctc aacgcccggg tgaagagcgt caggagggcc 2160
 gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc 2220
 gccatggtga agctcttccc ccgcctccgg gagatggggg ccgcatgct cctccaggtc 2280
 gccaacgagc tcctcctgga ggcccccaa gcgcgggccg aggaggtggc ggctttggcc 2340
 aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtggggatg 2400
 ggggaggact ggctttccgc caagggtcac caccaccacc accac 2445

<210> 580

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 580

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1				5					10					15	
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
65					70					75				80	
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
			85						90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val
			100					105						110	

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
 130 135 140
 Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
 145 150 155 160
 Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
 165 170 175
 Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
 180 185 190
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
 195 200 205
 Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
 210 215 220
 Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
 225 230 235 240
 Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255
 Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
 260 265 270
 Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
 275 280 285
 Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
 290 295 300
 Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
 305 310 315 320
 Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
 325 330 335
 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
 340 345 350
 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365
 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380
 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
 420 425 430
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445

Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480
 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
 530 535 540
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
 545 550 555 560
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 645 650 655
 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
 660 665 670
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 675 680 685
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 690 695 700
 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
 705 710 715 720
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
 725 730 735
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
 740 745 750
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
 755 760 765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
770 775 780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
785 790 795 800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
805 810 815

<210> 581

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 581

```

atgaattccc tgccctcttt tgagcccaag ggccgggtgc ttctggtgga cggccaccac      60
ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc      120
caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg      180
gtgatcgtgg tctttgacgc cgaggccccc tccttcgcgc accagaccta cgaggcctac      240
aaggcggggc gggctcccac ccccgaggac tttccccggc agcttgccct tatcaaggag      300
atggtggacc ttttgggctt taccgcctc gaggtgccgg gctttgaagc ggatgacgtc      360
ctggctaccc tggccaagaa ggcggaaaag gagggctacg aggtccgcat cctcaccgcc      420
gacaaagacc tttaccagct cctttccgac cgcattccacg tcctccaccc cgaggggtac      480
ctcatcacc cggcctggct ttgggaaaag tacggcctga ggcccgacca gtgggccgac      540
taccgggccc tgaccgggga cgagtccgac aaccttcccg gggtaaggga catcggggag      600
aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg      660
gaccggctga agcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc      720
tcctgggacc tggccaaggt gcgcaccgac ctgcccctgg aggtggactt cgccaaaagg      780
cgggagcccc accgggaggg ggagaagccc cgggaggagg ccccctggcc cccgcccga      840
ggggccttcg tgggcttcct cctttccgc cccgagccca tgtgggcgga gcttaaagcc      900
ctggccgctt gcaggggcgg ccgcgtgcac cgggcagcag accccttggc ggggctaaag      960
gacctcaagg aggtccgggg cctcctcgcc aaggacctcg ccgtcttggc ctcgaggag      1020
gggctagacc tcgtgcccgg ggacgacccc atgctcctcg cctacctcct ggacccttcg      1080
aacaccaccc ccgagggggg ggcgcggcgc tacggggggg agtggacgga ggacgccgcc      1140
caccgggccc tcctctcgga gaggtccat cggaacctcc ttaagcgctt cgagggggag      1200

```

gagaagctcc tttggctcta ccacgaggtg gaaaagcccc tctcccggt cctggcccat 1260
atggaggcca ccgggttacg gcgggacgtg gcctaccttc aggccctttc cctggagctt 1320
gcggaggaga tccgccgcct cgaggaggag gtcttccgct tggcgggcca ccccttcaac 1380
ctcaactccc gggaccagct ggaaaggggtg ctctttgacg agcttaggct tcccgcttg 1440
aagaagacga agaagacagg caagcgtcc accagcgccg cgggtgctgga ggccctacgg 1500
gagggccacc ccatcgtgga gaagatctc cagcaccggg agctcaccaa gctcaagaac 1560
acctacgtgg accccctccc aagcctcgtc cacccgagga cgggccgcct ccacaccgc 1620
ttcaaccaga cggccacggc cacggggagg cttagtagct ccgaccccaa cctgcagaac 1680
atccccgtcc gcacccctt gggccagagg atccgccggg ccttcgtggc cgaggcgggt 1740
tgggcggttg tggccctgga ctatagccag atagagctcc gcgtcctcgc ccacctctcc 1800
ggggacgaaa acctgatcag ggtcttccag gaggggaagg acatccacac ccagaccgca 1860
agctggatgt tcggcgctcc cccggaggcc gtggaccccc tgatgcgccg ggcgccaag 1920
acggtgaact tcggcgctct ctacggcatg tccgccata ggctctccca ggagcttgcc 1980
atccccctacg aggaggcggg ggcctttata gagcgctact tccaaagctt cccaaggtg 2040
cgggcctgga tagaaaagac cctggaggag gggaggaagc ggggctacgt ggaaaccctc 2100
ttcggaagaa ggcgctacgt gcccgaacct aacgcccggg tgaagagcgt cagggaggcc 2160
gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc 2220
gccatggtga agctcttccc ccgcctccgg gagatggggg ccgcgatgct cctccaggtc 2280
gccaacgagc tctcctgga gggcccccaa gcgcgggccc aggaggtggc ggctttggcc 2340
aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtggggatg 2400
ggggaggact ggctttccgc caagggtcac caccaccacc accac 2445

<210> 582

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 582

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1				5					10					15	
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		

- 748 -

Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380
 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr
 420 425 430
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445
 Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480
 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
 530 535 540
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
 545 550 555 560
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
 595 600 605
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
 625 630 635 640
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 645 650 655
 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
 660 665 670
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 675 680 685
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 690 695 700

Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
 705 710 715 720
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
 725 730 735
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
 740 745 750
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
 755 760 765
 Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
 770 775 780
 Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
 785 790 795 800
 Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
 805 810 815

<210> 583

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 583

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
 ggccaccacc tggcctaccg tacctttttt gccctgaagg gcctcaccac cagccggggg 120
 gagccggtcc aggcggtgta cggggttgcc aagagccttt tgaaggcgct aagagaagac 180
 ggggacgcgg tgatcgtggt ctttgacgcc gagggcccct ccttccgcca cgaggcctac 240
 ggggggtaca aggcggggcg ggctcccacc cccgaggact ttccccggca gcttgccctt 300
 atcaaggagc tgggtggacct cctgggggttt accgcctcgg aggtccccgg ctacgaggcg 360
 gacgacgttc tcgccaccct ggccaagaag gcggaaaagg aggggtacga ggtgcgcac 420
 ctcaccgccg acaaagacct ttaccagctc ctttccgacc gcatccacgt cctccacccc 480
 gaggggtacc tcatcaccac ggcttggttt tgggaaaagt acggcctgag gcccgaccag 540
 tgggcccact accgggccct gaccggggac gagtccgaca accttcccgg ggtcaagggc 600
 atcggggaga agaccgcct caagctcctc aaggagtggg ggagcctgga agccctcctc 660
 aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat 720
 ctgaagctct cctgggacct ggccaaggtg cgcaccgacc tgcccctgga ggtggacttc 780
 gccaaaaggc gggagcccga ccgggagggg ctttaaggcct ttttggagag gctggagttc 840

ggcagcctcc tccacgagtt cggcctcctg ggaggggaga agccccggga ggaggcccc	900
tggcccccg cggagggggc cttcgtgggc tttgtgcttt cccgcaagga gcccatgtgg	960
gccgatcttc tggccctggc cgcctgcagg ggcgcccgcg tgcaccgggc agcagacccc	1020
ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgccgtc	1080
ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgccctac	1140
ctcctggacc cttcgaacac ccccccgag ggggtggcgc ggcgctacgg gggggagtgg	1200
acggaggacg ccgcccaccg ggccctcctc tcggagaggc tccatcgga cctccttaag	1260
cgcctcgagg gggaggagaa gctcctttgg ctctaccacg aggtggaaaa gccctctcc	1320
cgggtcctgg cccatatgga ggccaccggg gtacggcggg acgtggccta ccttcaggcc	1380
ctttccctgg agcttgcgga ggagatccgc cgcctcgagg aggaggtctt ccgcttggcg	1440
ggccacccct tcaacctcaa ctcccgggac cagctggaaa gggtgctctt tgacgagctt	1500
aggcttcccg ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg	1560
ctggaggccc tacgggaggc ccaccccatc gtggagaaga tcctccagca ccgggagctc	1620
accaagctca agaacaccta cgtggacccc ctcccaagcc tcgtccaccg gaggacgggc	1680
cgcctccaca cccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac	1740
cccaacctgc agaacatccc cgtccgcacc cccttgggccc agaggatccg ccgggccttc	1800
gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gtcgccgctc	1860
ctcgcccacc tctccgggga cgaaaacctg atcagggctt tccaggaggg gaaggacatc	1920
cacaccacga ccgcaagctg gatgttcggc gtcccccccg aggccgtgga cccctgatg	1980
cgccgggcgg ccaagacggt gaacttcggc gtccctctacg gcatgtccgc ccataggctc	2040
tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa	2100
agcttcccca aggtgcgggc ctggatagaa aagaccctgg aggaggggag gaagcggggc	2160
tacgtgga aa cctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag	2220
agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc	2280
gacctcatga agctcgccat ggtgaagctc tcccccgcc tccgggagat gggggcccg	2340
atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag	2400
gtggcggtt tggccaagga ggccatggag aaggcctatc cctcgccgt gccctggag	2460
gtggagggtg ggatggggga ggactggctt tccgccaagg gtcaccacca ccaccaccac	2520

<210> 584

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 584

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Ala	Val
	50					55					60				
Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr
65					70					75				80	
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg
				85					90					95	
Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg
			100					105					110		
Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala
		115					120					125			
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp
	130					135					140				
Lys	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro
145					150					155					160
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu
			165						170					175	
Arg	Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser
			180					185					190		
Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys
		195					200					205			
Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp
	210					215						220			
Arg	Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp
225					230					235				240	
Leu	Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu
				245					250					255	

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
 305 310 315 320
 Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830
 Lys Gly His His His His His His
 835 840

<210> 585

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 585
atgaattccc tgccctctt tgagcccaag agccgggtgc ttctggtgga cggccaccac 60
ctggcctacc gcacctcctt cgccctgaag ggcctcacca ccagccgcgg ggagccggtg 120
cagatggtct acggcttcgc ccggagcctc ctcaaggcct tgaaggagga cggacaggcg 180
gtggtcgtgg tctttgacgc caaggcccc tcttccgcc acgaggccta cgaggcctac 240
aaggcggggc gggcccccac cccggaggac ttccccggca gctcgccctt atcaaggaga 300
tggtggacct tttgggcctg gcgcgcctcg aggtccccgg ctacgaggcg gacgacgttc 360
tcgccaccct ggccaagaag gcgaaaagg aggggtacga ggtgcgcatt ctaccgccga 420
ccgcgacctc taccaactcg tctccgaccg cgtcgccgtc ctccaccctg agggccacct 480
catcaccctg gagtggcttt gggagaagta cggcctcagg ccggagcagt ggggtggactt 540
ccgcgcctc gtgggggacc cctccgacaa cctccccggg gtcaagggca tcggggagga 600
gacggcggcc aagctgatcc gggagtgggg aagcctggaa aaccttctta agcacctgga 660
acaggcgaaa cctgcctccg tgcgggagaa gatccttagc cacatggagg acctcaagct 720
atccctggag ctatcccggg tgcacacgga cttgcttctt cagtggactt taaggccctg 780
cgccgcagga ccccgacct ggagggcctg agggcctttt tggaggagct ggagttcggc 840
agcctcctcc acgagttcgg cctcctggag gccccgcgg cggcggagga agctccctgg 900
ccgccccccg agggagcctt cgtgggggtac gttctttccc gccccgagcc catgtgggcg 960
gagcttaacg ccttgggcgc cgctggggc ggccgcgtgc accgggcagc agacccttg 1020
gcggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg 1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc 1140
ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200
gaggacgccc cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380
tccctggagc ttgcggagga gatccgcgc ctcgaggagg aggtcttccg cttggcgggc 1440
cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500
cttcccgct tgaagaagac gaagaagaca ggcaagcgt ccaccagcgc cgcggtgctg 1560
gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620
aagctcaaga acacctacgt ggacccccct ccaagcctcg tccaccgag gacggggcgc 1680
ctccacacc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740
aacctgcaga acatccccgt ccgcaccccc ttgggcccaga ggatccgccc ggccttcgtg 1800
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860

gcccacctct ccggggacga aaacctgac agggctcttc agggaggggaa ggacatccac 1920
 acccagaccg caagctggat gttcggcgtc cccccggagg ccgtggaccc cctgatgcgc 1980
 cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc 2040
 caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100
 ttccccaaag tgccggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160
 gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgccc ggtgaagagc 2220
 gtcaggagg cgcgggagcg catggccttc aacatgccc tccagggcac cgcgcgcgac 2280
 ctcatgaagc tcgccatggt gaagctcttc cccgcctcc gggagatggg ggcccgcgac 2340
 ctctccagg tcgccaacga gctcctcctg gaggcccccc aagcgcgggc cgaggaggtg 2400
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460
 gaggtgggga tgggggagga ctggctttcc gccaaaggt 2499

<210> 586

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 586

Met	Glu	Phe	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	1	5	10	15
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly	Leu	20	25	30	
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Gly	Asp	Arg	Asp	Leu	130	135	140	

Tyr Gln Leu Val Ser Asp Arg Val Ala Arg Pro Glu Gln Trp Val Asp
 145 150 155 160
 Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile Pro Gly Val Lys
 165 170 175
 Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp Gly Ser
 180 185 190
 Val Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala Ile Arg
 195 200 205
 Glu Lys Ile Leu Ala His Met Glu Asp Leu Lys Leu Ser Leu Glu Leu
 210 215 220
 Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val Asp Leu Ala Gln Gly
 225 230 235 240
 Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe Leu Glu Arg Leu Glu
 245 250 255
 Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Val Ala
 260 265 270
 Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Tyr
 275 280 285
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Asn Ala Leu Ala
 290 295 300
 Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly
 305 310 315 320
 Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala
 325 330 335
 Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro
 340 345 350
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
 355 360 365
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg
 370 375 380
 Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu
 385 390 395 400
 Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu
 405 410 415
 Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val
 420 425 430
 Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg
 435 440 445
 Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 450 455 460
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro
 465 470 475 480

Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 485 490 495
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 500 505 510
 Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu
 515 520 525
 Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 530 535 540
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 545 550 555 560
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 565 570 575
 Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln
 580 585 590
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 595 600 605
 Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp
 610 615 620
 Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 625 630 635 640
 Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 645 650 655
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile
 660 665 670
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 675 680 685
 Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly
 690 695 700
 Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg
 705 710 715 720
 Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 725 730 735
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg
 740 745 750
 Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu
 755 760 765
 Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu
 770 775 780
 Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
 785 790 795 800
 Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
 805 810

<210> 587

<211> 2433

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 587

```
atggaattcc tgccccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac      60
ctggcctacc gcaccttcca cgccctgaag ggccctacca ccagccgcgg ggagccggtc      120
caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagagaaga cggggatgtg      180
gtgatcgtgg tctttgacgc caaggccccc tccttcgcc acgaggccta cggggggtac      240
aaggcggggc ggcccccgac ccccgaggac tcccccggc agctcgccct catcaaggag      300
ctggtggacc tcctggggct ggcgcgcctc gaggtgccgg gctttgaagc ggatgacgtc      360
ctggctaccc tggccaagaa ggcggaaaag gagggtacg aggtgcgcat tctcaccggc      420
gaccgcgacc tttaaccaact cgtctccgac cgcgtcgcca ggccggagca gtgggtggac      480
taccgggcct tggccgggga cccttcgcac aacatccccg gcgtgaaggg catcggggag      540
aagacggcga ggaagcttct ggaggagtgg gggagcgtgg aagccctcct caagaacctg      600
gaccggctga agcccgccat ccgggagaag atcctggccc acatggagga cctcaagcta      660
tccttgagac tatcccggtt gcgcaccgac ctccccctgg aggtggacct cgcccagggg      720
cgggagcccc accgggaggg gcttaaggcc tttttggaga ggctggagtt cggaagcctc      780
ctccacgagt tcggcctgtt ggaaagcccc gtggcgggcg aggaagctcc ctggccgccc      840
cccgagggag ccttcgtggg gtacgttctt tcccgccccg agcccatgtg ggccggagctt      900
aacgccttgg ccgcgcctg gggcgggcgc gtgcaccggg cagcagaccc cttggcgggg      960
ctaaaggacc tcaaggaggt ccggggcctc ctgcceaagg acctcgccgt cttggcctcg     1020
agggaggggg tagacctcgt gcccggggac gaccccatgc tcctcgcta cctcctggac     1080
ccttcgaaca ccacccccga gggggtggcg cggcgctacg ggggggagtg gacggaggac     1140
gccgcccacc gggccctcct ctcgagagag ctccatcgga acctccttaa gcgcctcgag     1200
ggggaggaga agctcctttg gctctaccac gaggtggaaa agccctctc ccgggtcctg     1260
gcccataatg aggccaccgg ggtacggcgg gacgtggcct accttcagge cctttccctg     1320
gagcttgcgg aggagatccg ccgcctcgag gaggaggtct tccgcttggc gggccacccc     1380
ttcaacctca actcccggga ccagctggaa agggtgctct ttgacgagct taggcttccc     1440
gccttgaaga agacgaagaa gacaggcaag cgctccacca gcgcgcgggt gctggaggcc     1500
```

ctacgggagg cccaccccat cgtggagaag atcctccagc accgggagct caccaagctc 1560
 aagaacacct acgtggaccc cctcccaagc ctcgtccacc cgaggacggg ccgcctccac 1620
 acccgcttca accagacggc cacggccacg gggaggctta gtagctccga cccaacctg 1680
 cagaacatcc ccgtccgcac ccccttgggc cagaggatcc gccgggcctt cgtggccgag 1740
 gcgggttggg cgttgggtggc cctggactat agccagatag agtccgcgt cctcgccac 1800
 ctctccgggg acgaaaacct gatcagggtc ttccaggagg ggaaggacat ccacaccag 1860
 accgcaagct ggatgttcgg cgtccccccg gagggcgtgg acccctgat gcgccgggag 1920
 gccaagacgg tgaacttcgg cgtcctctac ggcatgtccg cccataggct ctcccaggag 1980
 cttgccatcc cctacgagga ggcggtggcc tttatagagc gctacttcca aagcttcccc 2040
 aaggtgcggg cctggataga aaagaccctg gagggagggga ggaagcgggg ctacgtggaa 2100
 accctcttcg gaagaaggcg ctacgtgccc gacctcaacg cccgggtgaa gagcgtcagg 2160
 gagggcgcgg agcgcattggc cttcaacatg cccgtccagg gcaccgccgc cgacctcatg 2220
 aagctcgcca tgggtgaagct cttccccccg ctccgggaga tggggggccg catgtctctc 2280
 caggtcgcca acgagctcct cctggaggcc cccaagcgc gggccgagga ggtggcggct 2340
 ttggccaagg aggccatgga gaaggcctat cccctcgccg tgcccctgga ggtggagggtg 2400
 gggatggggg aggactggct ttccgccaag ggt 2433

<210> 588

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 588

Met	Glu	Phe	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1				5					10				15		
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly	Leu
		20						25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly	Tyr
65					70					75				80	

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95
 Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val
 100 105 110
 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Gly Asp Arg Asp Leu
 130 135 140
 Tyr Gln Leu Val Ser Asp Arg Val Ala Arg Pro Glu Gln Trp Val Asp
 145 150 155 160
 Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile Pro Gly Val Lys
 165 170 175
 Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp Gly Ser
 180 185 190
 Val Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala Ile Arg
 195 200 205
 Glu Lys Ile Leu Ala His Met Glu Asp Leu Lys Leu Ser Leu Glu Leu
 210 215 220
 Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val Asp Leu Ala Gln Gly
 225 230 235 240
 Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe Leu Glu Arg Leu Glu
 245 250 255
 Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Val Ala
 260 265 270
 Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Tyr
 275 280 285
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Asn Ala Leu Ala
 290 295 300
 Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly
 305 310 315 320
 Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala
 325 330 335
 Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro
 340 345 350
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
 355 360 365
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg
 370 375 380
 Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu
 385 390 395 400
 Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu
 405 410 415

Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val
 420 425 430
 Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg
 435 440 445
 Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 450 455 460
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro
 465 470 475 480
 Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 485 490 495
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 500 505 510
 Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu
 515 520 525
 Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 530 535 540
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 545 550 555 560
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 565 570 575
 Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln
 580 585 590
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 595 600 605
 Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp
 610 615 620
 Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 625 630 635 640
 Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 645 650 655
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile
 660 665 670
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 675 680 685
 Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly
 690 695 700
 Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg
 705 710 715 720
 Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 725 730 735
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg
 740 745 750

Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu
755 760 765

Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu
770 775 780

Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
785 790 795 800

Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
805 810

<210> 589

<211> 2493

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 589

atgaattccc tgccctctt tgagcccaag ggccgggtcc tcctggtgga cggccaccac	60
ctggcctacc gtacctttt tgccctgaag ggctcacca cctcccgggg ggagccggtg	120
cagatggtct acggcttcgc ccggagcctc ctcaaggccc tcaaggagga cggggacgcg	180
gtgatcgtgg tctttgacgc cgaggccccc tccttcgcgc accagacctt cgaggcctac	240
aaggcgggga gggctccac ccccgaggac tttcccggc agcttgccct tatcaaggag	300
ctggtggacc tcctgggggt taccgcctc gaggtccccg gctacgaggc ggacgacgtt	360
ctcgccaccc tggccaagaa ggcggaag gagggctacg aggtgcgcat cctcaccgcg	420
gaccgggacc tttaccagct tctttccgac cgcattcacg tccttcaccc cgaggggtac	480
ctcatcaccc cggcctggct ttgggaaaag tacggcttga ggcccagcca gtgggcccgc	540
taccgggccc tgaccgggga cgaatccgac aacctttccg ggggtcaagg catcggggag	600
aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg	660
gaccggctga agcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc	720
tccttgagac tctcccgggt gcgcaccgac ctcctccctg aggtggactt cgccaaaagg	780
cgggagcccc accgggagag gcttagggcc tttctggaga ggcttgagtt tggcagcctc	840
ctccacgagt tcggcccttt ggaaagcccc agggccgcgg aggaagctcc ctggccgccc	900
cccgagggag ccttcgtggg gtacgttctt tcccgcctcg agcccatgtg ggcggagctt	960
aacgccttgg ccgcgccag gggcgccgc gtgcaccggg cagcagaccc cttggcgggg	1020
ctaaaggacc tcaaggaggt ccggggcctc ctgcgaagg acctcgccgt cttggcctcg	1080
agggaggggc tagacctcgt gcccggggac gaccccatgc tcctcgcta cctcctggac	1140

ccttcgaaca ccacccccga ggggggtggcg cggcgctacg gggggggagtg gacggaggac	1200
gccgcccacc gggccctcct ctcgagagag ctccatcgga acctccttaa gcgcctcgag	1260
ggggaggaga agctcctttg gctctaccac gaggtggaaa agcccctctc ccgggtcctg	1320
gcccataatgg aggccaccgg ggtacggcgg gacgtggcct accttcaggc cttttccctg	1380
gagcttgccg aggagatccg ccgcctcgag gaggaggtct tccgcttggc gggccacccc	1440
ttcaacctca actcccggga ccagctggaa agggtgctct ttgacgagct taggcttccc	1500
gccttgaaga agacgaagaa gacaggcaag cgctccacca gcgccgcggt gctggaggcc	1560
ctacgggagg cccaccccat cgtggagaag atcctccagc accgggagct caccaagctc	1620
aagaacacct acgtggaccc cctcccaagc ctcgctccacc cgaggacggg ccgcctccac	1680
accgccttca accagacggc cacggccacg gggaggctta gtagctccga ccccaacctg	1740
cagaacatcc ccgtccgcac ccccttgggc cagaggatcc gccgggcctt cgtggccgag	1800
gcgggttggg cgttggtggc cctggactat agccagatag agctccgcgt cctcgccac	1860
ctctccgggg acgaaaacct gatcagggtc ttccaggagg ggaaggacat ccacaccag	1920
accgcaagct ggatgttcgg cgtccccccg gaggccgtgg accccctgat gcgccgggcg	1980
gccaagacgg tgaacttcgg cgtcctctac ggcatgtccg cccataggct ctcccaggag	2040
cttgccatcc cctacgagga ggcggtggcc tttatagagc gctacttcca aagcttcccc	2100
aagggtgcggg cctggataga aaagaccctg gaggagggga ggaagcgggg ctacgtggaa	2160
accctcttcg gaagaaggcg ctacgtgccg gacctcaacg cccgggtgaa gagcgtcagg	2220
gaggccgcgg agcgcattgg cttcaacatg cccgtccagg gcaccgccgc cgacctcatg	2280
aagctcgcca tggatgaagct cttccccgc ctccgggaga tgggggcccg catgctcctc	2340
caggctcgcca acgagctcct cctggaggcc ccccaagcgc gggccgagga ggtggcggct	2400
ttggccaagg aggccatgga gaaggcctat cccctcgccg tgcccctgga ggtggagggtg	2460
gggatggggg aggactggct ttccgccaag ggt	2493

<210> 590

<211> 831

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 590

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	1	5	10	15
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu	20	25	30	
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Met	Val	Tyr	Gly	Phe	Ala	Arg	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu	130	135	140	
Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly	Tyr	145	150	155	160
Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Asp	165	170	175	
Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn	Leu	180	185	190	
Ser	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	Glu	195	200	205	
Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	Lys	210	215	220	
Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys	Leu	225	230	235	240
Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp	245	250	255	
Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	Phe	Leu	260	265	270	
Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Pro	Leu	Glu	275	280	285	
Ser	Pro	Arg	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	290	295	300	
Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu	305	310	315	320

Asn Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Ala Asp
 325 330 335
 Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala
 340 345 350
 Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro
 355 360 365
 Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr
 370 375 380
 Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp
 385 390 395 400
 Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu
 405 410 415
 Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val
 420 425 430
 Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val
 435 440 445
 Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu
 450 455 460
 Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro
 465 470 475 480
 Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
 485 490 495
 Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser
 500 505 510
 Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
 515 520 525
 Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr
 530 535 540
 Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His
 545 550 555 560
 Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
 565 570 575
 Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
 580 585 590
 Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu
 595 600 605
 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
 610 615 620
 Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln
 625 630 635 640
 Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu
 645 650 655

Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met
 660 665 670
 Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala
 675 680 685
 Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala
 690 695 700
 Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu
 705 710 715 720
 Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val
 725 730 735
 Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
 740 745 750
 Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe
 755 760 765
 Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn
 770 775 780
 Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala
 785 790 795 800
 Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu
 805 810 815
 Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly
 820 825 830

<210> 591

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 591

agaaaggaag ggaagaaagc gaa

23

<210> 592

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 592

tggagggtcaa aacatcgata agtcgaagaa aggaagggaa gaaat

45

<210>	593	
<211>	14	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	593	
	tgttttgacc tcca	14
<210>	594	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	594	
	ggcgaccaca cccgtcctgt	20
<210>	595	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	595	
	ccacgatgcg tccggcgtag	20
<210>	596	
<211>	26	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	596	
	acgggtcaat gtccatgccc caaaga	26

<210> 597
 <211> 41
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (23)..(23)
 <223> /note= "The residue at this position indicates 2' o-methyl sugar"
 <400> 597
 gtctgagatg aaagtgctcc cgcacccacc caaggcacag c 41
 <210> 598
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 598
 tcttcgcaca tttcatctca gacgga 26
 <210> 599
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(17)
 <223> /note= "The residues at these positions are 2' o-methyl sugars"
 <400> 599
 gctgtgcctt ggggtggg 17

<210> 600
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(21)
 <223> /note= "The residues at these positions are 2' o-methyls"
 <400> 600
 gctgtgcctt ggggtgggtgc g 21
 <210> 601
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 601
 aacgagggcgc acccacccaa ggcacagc 28
 <210> 602
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (23)..(27)
 <223> /note= "The residues at these positions are 2' o-methyls"
 <400> 602
 gtctgagatg aaagtgcgcc tcgttaa 27

<210>	603	
<211>	28	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	603	
	aacgaggcgc acccacccaa ggcacagc	28
<210>	604	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	604	
	tcttcgcaca ttccatctca gac	23
<210>	605	
<211>	21	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	605	
	gctgtgcctt ggggtgggtgc g	21
<210>	606	
<211>	26	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	606	
	tcttcgcaca ttccatctca gacgga	26

<210> 607
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 607
 gctgtgcctt ggggtgggtgc 20
 <210> 608
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (15)..(20)
 <223> /note= "The residues at these positions are 2' o-methyl sugars"
 <400> 608
 gctgtgcctt ggggtgggtgc 20
 <210> 609
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(20)
 <223> /note= "The residues at these positions are 2' o-methyl sugars"
 <400> 609
 gctgtgcctt ggggtgggtgc 20

<210> 610
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 610
 acgggtcaat gtccatgcc caaaga 26
 <210> 611
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 611
 aacgaggcgc acccacccaa ggcacagc 28
 <210> 612
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (23)..(27)
 <223> /note= "The residues at these positions are 2' o-methyls"
 <400> 612
 gtctgagatg aaagtgcgcc tcgttaa 27
 <210> 613
 <211> 17
 <212> DNA

```

<213> Artificial Sequence
<220>
<223> Synthetic
<220>
<221> modified_base
<222> (1)..(17)
<223> /note= "The residues at these positions are 2' o-methyls"
<400> 613
gctgtgcctt ggggtggg
17
<210> 614
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic
<220>
<221> modified_base
<222> (1)..(19)
<223> /note= "The residues at these positions are 2' o-methyls"
<400> 614
gctgtgcctt ggggtgggtg
19
<210> 615
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic
<220>
<221> modified_base
<222> (1)..(21)
<223> /note= "The residues at these positions are 2' o-methyls"
<400> 615
gctgtgcctt ggggtgggtgc g
21

```

<210> 616
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(22)
 <223> /note= "The residues at these positions are 2' o-methyls"
 <400> 616
 gctgtgcctt ggggtgggtgc gc 22
 <210> 617
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 617
 ccgtcaacat ttaccatggg tgcgga 26
 <210> 618
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 618
 ccgccacctc gtagtcgaca tccttttctg g 31
 <210> 619
 <211> 29
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 619

ttgataaaatt tggggtggaa aggtttgga

29

<210> 620

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 620

agaactgaga ggaggcg

17

<210> 621

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 621

aacgaggcgc accaaactca ctcat

25

<210> 622

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 622

gtcatgtagg cttctatgta gttgatgaag atgta

35

<210> 623

<211> 26

<212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 623
 ggctttgtag atgcctttct cttgga 26
 <210> 624
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 624
 atgagtgagt ttggtgcg 18
 <210> 625
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 625
 ccaggaagca agtggtgcgc ctcgttt 27
 <210> 626
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 626
 aacgaggcgc accttggagg ca 22
 <210> 627
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 627
aaggtttcct tctcagttgt gtta

24

<210> 628

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 628
gcaaagatgt ctgttacggt caactc

26

<210> 629

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 629
tgcctccaag gtgcgc

16

<210> 630

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 630
aacgaggcgc accttcaaaa tgcctaa

27

<210> 631

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 631

tgtcactctc ctctttccaa tta

23

<210> 632

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 632

gaaaagagtt ccattatccg ctacatctg

29

<210> 633

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 633

ttaggcattt tgaaggtgcg c

21

<210> 634

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 634

aacgaggcgc accgttgtgt ccc

23

<210> 635

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 635

gggatgtaga agccattcag a

21

<210> 636

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 636

ttgttggtgct gtgggggatg

20

<210> 637

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 637

gggacacaac ggtgcgc

17

<210> 638

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 638

ccgtcacgcc tccaccatat ccc

23

<210> 639

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 639

ccagcggttt ccattggcaa agatcaa

27

<210> 640

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 640

cggaagaatg ggtcgaccat g

21

<210> 641

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 641

gggatatggt ggaggcg

17

<210> 642

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 642

aacgaggcgc accgttccag gc

22

<210> 643

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 643

catatccatg cagcaccacc atga

24

<210> 644

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 644

caaaatacag agtgaacaca gggcc

25

<210> 645

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 645

gcctggaacg gtgcgc

16

<210> 646

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 646

ccgtcacgcc tcatggataa tgccc

25

<210> 647

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 647

caggtgagaa aaggcattac agatagtgaa agc

33

<210> 648

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 648

cagaggaaag agagctgcag gg

22

<210> 649

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 649

gggcattatc catgaggcg

19

<210> 650

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 650

ccgtcacgcc tccctgctga gaaa

24

<210> 651

<211> 20

<212> DNA

<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 651	
cccgagcat gcacggcgga	20
<210> 652	
<211> 15	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 652	
ggcaggaagg cctcc	15
<210> 653	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 653	
tttctcagca gggaggcg	18
<210> 654	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 654	
ccgtcacgcc tcgccccaca	20
<210> 655	
<211> 28	
<212> DNA	

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 655

cagcacaggc tggtgaccat cataaaac

28

<210> 656

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 656

cttttccata ctttttatga cattc

25

<210> 657

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 657

tgtggggcga ggcg

14

<210> 658

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 658

aacgaggcgc acagttgacc ttc

23

<210> 659

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 659

gtgatggcca gcacagggc

19

<210> 660

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 660

atacgttccc cacatttttc

20

<210> 661

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 661

tgaaggtcaa ctgtgcgc

18

<210> 662

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 662

aacgaggcgc acgtcataaa tacccc

26

<210> 663

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 663

gccagcatag gctgttgaca c

21

<210> 664

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 664

agacttttct atacttttta taacattc

28

<210> 665

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 665

gggggtattta tgacgtgcgc

20

<210> 666

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 666

ccgtcacgcc tctgtctgt gat

23

<210> 667

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 667

tcctgacagt gctcaatcag ga

22

<210> 668

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 668

tcctgacaat gctcaatgag ga

22

<210> 669

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 669

gtcccggatg tggccc

16

<210> 670

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 670

atcacagaca ggaggcg

17

<210> 671

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 671

aacgaggcgc acggactggt ttctgc

26

<210> 672

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 672

cttgtcaaag tcttgatagt gctcctc

27

<210> 673

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 673

cttgttgaag tcttgatagt gttcctc

27

<210> 674

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 674

gcagaaaaca gtccgtgcgc

20

<210> 675

<211> 23

<212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 675
 ccgtcacgcc tcaactgcggt cat 23
 <210> 676
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 676
 gtggataact gcatcagtgt atggcatttt c 31
 <210> 677
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 677
 caagggttgg tagcctgtgt gagcc 25
 <210> 678
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 678
 atgaccgcag tgaggcg 17
 <210> 679
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 679

ccgtcacgcc tcagagccaa tcac

24

<210> 680

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 680

cgatcatcaa gggatgggtgg cctgtgc

27

<210> 681

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 681

ctgatcaatc tccttttggga ctttctctgc g

31

<210> 682

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 682

gtgattggct ctgaggcg

18

<210> 683

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 683

ccgtcacgcc tcctcttcaa tttctg

26

<210> 684

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 684

ccctgtcaat ttcttcatga agttta

26

<210> 685

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 685

ggtatttcat gaggatcagg agc

23

<210> 686

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 686

cagaaattga agaggaggcg

20

<210> 687

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 687

aacgaggcgc accgggtccc a

21

<210> 688

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 688

tcccctgttt cttgaaaagt ccatgtgtga

30

<210> 689

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 689

aatccgtaga ggagcaccag g

21

<210> 690

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 690

tgggacccgg tgcgc

15

<210> 691

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 691

ccgtcacgcc tcctcggcag g

21

<210> 692

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 692

cacaatatcg taggtaggag gtgccttaa

29

<210> 693

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 693

gccccatcga tctcctcc

18

<210> 694

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 694

cctgccgagg aggcg

15

<210> 695

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 695
aacgaggcgc actaggcttt gct

23

<210> 696

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 696
ttcatgtagt cagggtcata gacaattaag a

31

<210> 697

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 697
tccccagaac catcgaggaa agg

23

<210> 698

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 698
agcaaagcct agtgcgc

17

<210> 699

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 699

aacgaggcgc acagaaggcc cctt

24

<210> 700

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 700

ccttgaacag caccagaaat agactgagca c

31

<210> 701

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 701

ggaagaaccc agagacacca tcc

23

<210> 702

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 702

aaggggcctt ctgtgcgc

18

<210> 703

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 703

aacgagggcgc acgttgatgac acctt

25

<210> 704

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 704

gatgaaggcc ataaattaaa attgtgc

27

<210> 705

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 705

tgggtatgga acgtcc

16

<210> 706

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 706

aaggtatcac aacgtgcgc

19

<210> 707

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 707

cccccttttg gggg

14

<210> 708

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 708

ccctatcttt aaagttttta aaaagtttga

30

<210> 709

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 709

ccgccgagat cactctgact gcct

24

<210> 710

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 710

ttgtcactcg gggttcgaga agatgaa

27

<210> 711

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 711

gggccagagg gctgattag

19

<210> 712

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 712

gggccagagg gctgatta

18

<210> 713

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 713

gggccagagg gctgat

16

<210> 714

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 714

gggccagagg gct

13

<210> 715

<211> 11

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 715
gggccagagg g

11

<210> 716

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 716
aggcagtcag agtgatc

17

<210> 717

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 717
aggcagtcag agtgatctc

19

<210> 718

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 718
cggaagaagc agttggtgat ctcggcgg

28

<210> 719

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 719
caacgcttcc tccg

14

<210> 720

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 720
ccgtcacgcc tctctgactg cct

23

<210> 721

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 721
ttgtcactcg gggttcgaga agatgaa

27

<210> 722

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 722
gggccagagg gctgattag

19

<210> 723
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 723
 aggcagtcag agaggcg 17
 <210> 724
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 724
 cggaagaagc agttggaggc gtgacggt 28
 <210> 725
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 725
 caacgcttcc tccg 14
 <210> 726
 <211> 25
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 726

ccgtcacgcc tctctgactg cctgg

25

<210> 727

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 727

ttgtcactcg gggttcgaga agatgaa

27

<210> 728

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 728

ccaggcagtc agagaggcg

19

<210> 729

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 729

cggaagaagc agttggaggc gtgacggt

28

<210> 730

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 730

caacgcttcc tccg

14

<210> 731

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 731

ccgccgagat cactctgact gcc

23

<210> 732

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 732

ttgtcactcg gggttcgaga agatgaa

27

<210> 733

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 733

tgggccagag ggctgatta

19

<210> 734
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 734
 aggcagtcag agtgatc 17
 <210> 735
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 735
 cggaagaagc agttggtgat ctcggcgg 28
 <210> 736
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 736
 caacgcttcc tccg 14
 <210> 737
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 737

ccgccgagat cactgatctg actg

24

<210> 738

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 738

cttgctactc ggggttcgag aagac

25

<210> 739

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 739

cctgggccag agggctgatt

20

<210> 740

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 740

cagtcagatc agtgatc

17

<210> 741

<211> 28

<212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 741
 cggaagaagc agttggtgat ctcggcgg 28
 <210> 742
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 742
 caacgcttcc tccg 14
 <210> 743
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 743
 ccgtcacgcc tctctgactg cca 23
 <210> 744
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 744
 ccgtcacgcc tctctgactg ccg 23

<210> 745
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 745
 ccgtcacgcc tctctgacgg cct 23
 <210> 746
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 746
 ccgtcacgcc tctctgacag cct 23
 <210> 747
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 747
 ttgtcactcg gggttcgaga agatgaa 27
 <210> 748
 <211> 11
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 748
 gggccagagg g 11

<210>	749	
<211>	17	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	749	
	aggcagtcag agaggcg	17
<210>	750	
<211>	17	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	750	
	aggccgtcag agaggcg	17
<210>	751	
<211>	17	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	751	
	aggctgtcag agaggcg	17
<210>	752	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	752	
	ccaggaagca agtggaggcg tgacggu	27

<210> 753
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
 <400> 753
 cactgcttcg tgg 13
 <210> 754
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 754
 ccgccgagat cactctgatg cctggg 26
 <210> 755
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 755
 cttgtcactc ggggttcgag aagatgaa 28
 <210> 756
 <211> 20
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 756
 cccaggcagt cagagtgatc 20
 <210> 757
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 757
 cggaggaagc agttggtgat ctcggcgg 28
 <210> 758
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 758
 caacgcttcc tccg 14
 <210> 759
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 759
 ccgtcacgcc tccatctggt taggg 25

<210> 760
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 760
 caggtcctgg aaggagcact ta 22
 <210> 761
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 761
 ccatcagctt ctttgttctt gtcac 26
 <210> 762
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 762
 gccctaaaca gatggaggcg 20
 <210> 763
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 763
 cggaagaagc agttggaggc gtgacggt 28

<210> 764
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 764
 caacgcttcc tccg 14
 <210> 765
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 765
 ccgtcacgcc tccatctgtt tagggc 26
 <210> 766
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 766
 caggtcctgg aaggagcact ta 22
 <210> 767
 <211> 26
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 767

catcagcttc tttgttcttg tcatcc

26

<210> 768

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 768

gccctaaaca gatggaggcg

20

<210> 769

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 769

cggaagaagc agttggaggc gtgacggt

28

<210> 770

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 770

caacgcttcc tccg

14

<210> 771

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 771

ccgtcacgcc tccatctgtt tagg

24

<210> 772

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 772

caggtcctgg aaggagcact ta

22

<210> 773

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 773

gccatcagct tctttgttct tgatc

27

<210> 774

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 774

cggaagaagc agttggaggc gtgacggt

28

<210> 775

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 775
caacgcttcc tccg

14

<210> 776

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 776
ccgtcacgcc tcccatcagc ttc

23

<210> 777

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 777
gagcacttca tctgtttagg ga

22

<210> 778

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 778
tttgttcttg tcatactcat tgccac

26

<210> 779
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 779
 gaagctgatg ggaggcg 17
 <210> 780
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 780
 cggaagaagc agttggaggc gtgacggt 28
 <210> 781
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 781
 caacgcttcc tccg 14
 <210> 782
 <211> 29
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 782

ccgccgagat cactcatctg tttagggcc

29

<210> 783

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 783

ccgccgagat cactcatctg tttagggc

28

<210> 784

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 784

caggtcctgg aaggagcact a

21

<210> 785

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 785

ggccctaaac agatgagtga tc

22

<210> 786

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 786

cggaggaagc agttggtgat ctcggcgg

28

<210> 787

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 787

caacgcttcc tccg

14

<210> 788

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 788

ccgtcacgcc tccagcaggt tggc

24

<210> 789

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 789

gcttgaccca gggaggg

17

<210> 790

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 790

gccaaaggtgc tggaggcg

18

<210> 791

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 791

cggaagaagc agttggaggc gtgacggt

28

<210> 792

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 792

caacgcttcc tccg

14

<210> 793

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 793

ccgtcacgcc tccagcaggt tgg

23

<210> 794

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 794

gcttgaccca gggaggg

17

<210> 795

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 795

caatctcggg ctgcaaagca gac

23

<210> 796

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 796

gccaaggtgc tggaggcg

18

<210> 797

<211> 28

<212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 797
 cggaagaagc agttggaggc gtgacggt 28
 <210> 798
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 798
 caacgcttcc tccg 14
 <210> 799
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 799
 ccgtcacgcc tctcagcagg ttgg 24
 <210> 800
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 800
 actctagttt ttccttctcc ta 22

<210> 801

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 801

caatctcggg ctgcaaagca gac

23

<210> 802

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 802

ccaacctgct gagaggcg

18

<210> 803

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 803

cggaagaagc agttggaggc gtgacggt

28

<210> 804

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 804
 caacgcttcc tccg 14
 <210> 805
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 805
 ccgccgagat cactctcctc attgaatcct 30
 <210> 806
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 806
 ccgccgagat cactctcctc attgaatcc 29
 <210> 807
 <211> 34
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 807
 ccaaaagtcc agtgatgatt ttcaccaggc aaga 34
 <210> 808
 <211> 25
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 808
 aggattcaat gaggaagagt gatct 25
 <210> 809
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 809
 cggaggaagc agttggtgat ctcggcgg 28
 <210> 810
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 810
 caacgcttcc tccg 14
 <210> 811
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 811
 ccgtcacgcc tcctcctcat tgaa 24

<210> 812

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 812

ccagtgatga ttttcaccag gcaagta

27

<210> 813

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 813

tccagattgg aagcatccat ct

22

<210> 814

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 814

ttcaatgagg aggaggc

17

<210> 815

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 815

cggaagaagc agttggaggc gtgacggt

28

<210> 816
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 816
 caacgcttcc tccg 14
 <210> 817
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 817
 ccgtcacgcc tctctctcat tga 23
 <210> 818
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 818
 ccagtgatga ttttcaccag gcaagta 27
 <210> 819
 <211> 23
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 819
 atccagattg gaagcatcca tct 23
 <210> 820
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 820
 ttcaatgagg aggaggc 17
 <210> 821
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 821
 cggaagaagc agttggaggc gtgacggt 28
 <210> 822
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 822
 caacgcttcc tccg 14

<210>	823	
<211>	26	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	823	
	ccgtcacgcc tcctcctcat tgaatg	26
<210>	824	
<211>	26	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	824	
	ccgtcacgcc tcctcctcat tgaata	26
<210>	825	
<211>	26	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	825	
	ccgtcacgcc tcctcctcat tgaatt	26
<210>	826	
<211>	35	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	826	
	ccaaaagtcc agtgatgatt ttcaccaggc aagta	35

<210> 827
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 827
 cagattggaa gcatccatct 20
 <210> 828
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 828
 gattcaatga ggaggaggc 19
 <210> 829
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 829
 ccaggaagca agtggaggcg tgacggg 27
 <210> 830
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>

<221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
 <400> 830
 cactgcttcg tgg 13
 <210> 831
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 831
 ccgtcacgcc tccttcggag tttggt 26
 <210> 832
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 832
 ccgtcacgcc tccttcggag tttggtt 27
 <210> 833
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 833
 gggttgtgga gtgagtgttc aagta 25
 <210> 834
 <211> 24
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 834
 aacccaaact ccgaaggcgg cgtg 24
 <210> 835
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 835
 cggaagaagc agttggaggc gtgacggt 28
 <210> 836
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 836
 caacgcttcc tccg 14
 <210> 837
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 837
 gccgtcacgc ctctttgggt ttgcttgtc 29

<210> 838
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 838
 gccgtcacgc ctctttgggt ttgcttgt 28
 <210> 839
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 839
 tggagtgagt gttcaagtct tcggaga 27
 <210> 840
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 840
 gacaagcaaa cccaaagagg cg 22
 <210> 841
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 841
 cggaagaagc agttggaggc gtgacggc 28

<210> 842
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 842
 caacgcttcc tccg 14
 <210> 843
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 843
 cctgtctcgc tgccttcgga gtttggg 27
 <210> 844
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 844
 cctgtctcgc tgccttcgga gtttgg 26
 <210> 845
 <211> 25
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 845
 gggttgtgga gtgagtgttc aagta 25
 <210> 846
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 846
 cccaaactcc gaaggcagcg 20
 <210> 847
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 847
 cggaggaagc agttggcagc gagacagg 28
 <210> 848
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (26)..(26)
 <223> The modified nucleotide at this position is amino-deoxy adenosine
 <400> 848
 cggaggaagc agttggcagc gagacagg 28

<210> 849

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (22)..(22)

<223> The modified nucleotide at this position is amino-deoxy adenosine

<400> 849

cggaggaagc agttggcagc gagacagg

28

<210> 850

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (18)..(18)

<223> The modified nucleotide at this position is amino-deoxy adenosine

<400> 850

cggaggaagc agttggcagc gagacagg

28

<210> 851

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (22)..(22)

<223> The modified nucleotide at this position is amino-deoxy adenosine

<220>

<221> modified_base

<222> (26)..(26)

<223> The modified nucleotide at this position is amino-deoxy adenosine

<400> 851

cggaggaagc agttggcagc gagacagg

28

<210> 852

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (18)..(18)

<223> The modified nucleotide at this position is amino-deoxy adenosine

<220>

<221> modified_base

<222> (26)..(26)

<223> The modified nucleotide at this position is amino-deoxy adenosine

<400> 852

cggaggaagc agttggcagc gagacagg

28

<210> 853

<211> 28

<212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (18)..(18)
 <223> The modified nucleotide at this position is amino-deoxy adenosine
 <220>
 <221> modified_base
 <222> (22)..(22)
 <223> The modified nucleotide at this position is amino-deoxy adenosine
 <400> 853
 cggaggaagc agttggcagc gagacagg 28
 <210> 854
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 854
 caacgcttcc tccg 14
 <210> 855
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 855
 gccgtcacgc ctctgggaca cttgctgc 28
 <210> 856
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 856
 gccacaatgg tcttgaagat cacagcttct ta 32
 <210> 857
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 857
 gcagcaagtg tcccagaggc g 21
 <210> 858
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 858
 cggaagaagc agttggaggc gtgacggc 28
 <210> 859
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>

<221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 859
 caacgcttcc tccg 14
 <210> 860
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 860
 ccgtcacgcc tccttcggag tttggg 26
 <210> 861
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 861
 gggttgtgga gtgagtgttc aagta 25
 <210> 862
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 862
 gggaaactcc gaaggaggcg 20
 <210> 863
 <211> 27
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 863
 ccaggaagca agtggaggcg tgacggu 27
 <210> 864
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
 <400> 864
 cactgcttcg tgg 13
 <210> 865
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 865
 cgccgagatc accttcggag tttggg 26
 <210> 866
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 866
 gggttgtgga gtgagtgttc aagta 25

<210> 867
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 867
 cccaaactcc gaaggtgatc 20
 <210> 868
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 868
 cggaagaagc agttggtgat ctggcg 28
 <210> 869
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 869
 caacgcttcc tccg 14
 <210> 870
 <211> 26
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 870

aacgaggcgc accttcggag tttggg

26

<210> 871

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 871

gggttggtgga gtgagtgttc aagta

25

<210> 872

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 872

cccaaactcc gaaggtgcg

19

<210> 873

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 873

cggaagaagc agttggtgcg cctcgtaa

29

<210> 874

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 874
caacgcttcc tccg

14

<210> 875

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 875
ccgtcacgcc tccttcggag tttgg

25

<210> 876

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 876
gggttggtga gtgagtgttc aagta

25

<210> 877

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 877
gtttgcttgt ccaggtgg

18

<210> 878

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 878

ccaaactccg aaggaggcg

19

<210> 879

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 879

cggaagaagc agttggaggc gtgacggt

28

<210> 880

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 880

caacgcttcc tccg

14

<210> 881

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 881

ccgtcacgcc tccttcggag tttg

24

<210> 882

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 882

gggttggtga gtgagtgttc aagta

25

<210> 883

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 883

gttttgcttg tccaggtgg

19

<210> 884

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 884

ccaaactccg aaggaggcg

19

<210> 885

<211> 28

<212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 885
 cggaagaagc agttggaggc gtgacggt 28
 <210> 886
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 886
 caacgcttcc tccg 14
 <210> 887
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 887
 ccgtcacgcc tccttcggag ttt 23
 <210> 888
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 888
 gggttgtgga gtgagtgttc aagta 25

<210> 889

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 889

gggtttgctt gtccaggtg

19

<210> 890

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 890

ccaaactccg aaggaggcg

19

<210> 891

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 891

cggaagaagc agttggaggc gtgacggt

28

<210> 892

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 892
 caacgcttcc tccg 14
 <210> 893
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 893
 ccgtcacgcc tccggagttt ggg 23
 <210> 894
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 894
 gttgtggagt gagtgttcaa gtatta 26
 <210> 895
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 895
 tttgcttgtc caggtggtcc ag 22

<210> 896

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 896

cccaaactcc ggaggcg

17

<210> 897

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 897

cggaagaagc agttggaggc gtgacggt

28

<210> 898

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 898

caacgcttcc tccg

14

<210> 899

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 899
cgccgagatc accggagttt ggg

23

<210> 900

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 900
gttgtggagt gagtgttcaa gtatta

26

<210> 901

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 901
tttgcttgtc caggtggtcc ag

22

<210> 902

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 902
ctagtggcct caaaccc

17

<210> 903

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 903
cggaagaagc agttggtgat ctcggcgg

28

<210> 904

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3
dye

<400> 904
caacgcttcc tccg

14

<210> 905

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 905
cgccgagatc acctttacat tttctatcgt

30

<210> 906

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 906
cgccgagatc acctttacat tttctatcgt

30

<210> 907

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 907

ccttccttat cctggatcct ggca

24

<210> 908

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 908

acgatagaaa atgtaaaggt gatc

24

<210> 909

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 909

cgcagtgaga atgaggtgat ctcggcggt

29

<210> 910

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
 <400> 910
 ctcttctcag tgcg 14
 <210> 911
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 911
 gtttcttttg tgtctccgca ctgcc 25
 <210> 912
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 912
 ccagcagtaa atgctccagt tgtaga 26
 <210> 913
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 913
 tagaacttga agtaggtgc 19
 <210> 914
 <211> 19
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 914
caaagaaaac acaggaggc

19

<210> 915

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 915
ccaggaagca agtggaggcg tgacggu

27

<210> 916

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (3)..(3)

<223> The residue at this position is linked to a Z21 quenching group.

<400> 916
cactgcttcg tgg

13

<210> 917

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 917
aacgaggcgc acctgtgttt tctttg

26

<210> 918
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 918
 ccagcagtaa atgctccagt tgtaga 26
 <210> 919
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 919
 tagaacttga agtaggtgc 19
 <210> 920
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 920
 caaagaaaac acaggtgcg 19
 <210> 921
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 921
 ccaggaagca agtggtgcgc ctcgttt 27

<210> 922
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
 <400> 922
 cactgcttcg tgg 13
 <210> 923
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 923
 ccgtcacgcc tcctccagtt gtag 24
 <210> 924
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 924
 aaaatcatct gttaaaccag cagtaaata 30
 <210> 925
 <211> 20
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 925

ctgtgttttc tttgtagaac

20

<210> 926

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 926

ctacaactgg aggaggc

17

<210> 927

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 927

ccaggaagca agtggaggcg tgacggg

27

<210> 928

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (3)..(3)

<223> The residue at this position is linked to a Z21 quenching group.

<400> 928

cactgcttcg tgg

13

<210> 929
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 929
 aacgaggcgc acctccagtt gtag 24
 <210> 930
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 930
 aaaatcatct gttaaaccag cagtaaata 30
 <210> 931
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 931
 ctgtgttttc tttgtagaac 20
 <210> 932
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 932
 ctacaactgg aggtgcg 17

<210> 933
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 933
 ccaggaagca agtgggtgcgc ctcgttt 27
 <210> 934
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
 <400> 934
 cactgcttcg tgg 13
 <210> 935
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 935
 ccgtcacgcc tcctgtgttt tctttgta 28
 <210> 936
 <211> 32
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 936

gtaaatccag cagtaaattgc tccagttgta ga

32

<210> 937

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 937

gaacttgaag taggtgcact gtt

23

<210> 938

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 938

tacaaagaaa acacaggagg cgt

23

<210> 939

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 939

ccaggaagca agtggaggcg tgacggg

27

<210> 940

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (3)..(3)

<223> The residue at this position is linked to a Z21 quenching group.

<400> 940

cactgcttcg tgg

13

<210> 941

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 941

aacgaggcgc acctgtgttt tctttgta

28

<210> 942

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 942

gtaaatccag cagtaaattgc tccagttgta ga

32

<210> 943

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 943

gaacttgaag taggtgcact gtt

23

<210> 944
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 944
 tacaaagaaa acacaggtgc g 21
 <210> 945
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 945
 ccaggaagca agtgggtgcgc ctcgttt 27
 <210> 946
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
 <400> 946
 cactgcttcg tgg 13
 <210> 947
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 947

ccgtcacgcc tcctccagtt gtaa

24

<210> 948

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 948

ccgtcacgcc tcctccagtt gtat

24

<210> 949

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 949

ccgtcacgcc tcctccagtt gtac

24

<210> 950

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 950

aaaatcatct gtaaattccag cagtaaatga

30

<210> 951

<211> 20

<212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 951
 ctgtgttttc tttgtagaac 20
 <210> 952
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 952
 ctacaactgg aggaggc 17
 <210> 953
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 953
 ccaggaagca agtggaggcg tgacggg 27
 <210> 954
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
 <400> 954
 cactgcttcg tgg 13

<210> 955
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 955
 gccgtcacgc ctcccttctt gatg 24
 <210> 956
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 956
 ttctagacac tgaagatggt tcagttctgt gga 33
 <210> 957
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 957
 catgcccgaag aaggaggcgcg 20
 <210> 958
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 958
 cggaagaagc agttggaggc gtgacggc 28

<210> 959
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 959
 caacgcttcc tccg 14
 <210> 960
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 960
 ccgtcacgcc tctaattcca ttcaaaatca tct 33
 <210> 961
 <211> 34
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 961
 catcctgggtg agtttgggat tcttgtaatt tata 34
 <210> 962
 <211> 25
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 962

gtaaatccag cagtaaattgc tccag

25

<210> 963

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 963

agatgatttt gaatggaatt agaggcg

27

<210> 964

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 964

cggaagaagc agttggaggc gtgacggc

28

<210> 965

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 965

caacgcttcc tccg

14

<210> 966
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 966
 ccgccgagat cacctgtggt ttctttgta 29
 <210> 967
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 967
 gtaaatccag cagtaaatgc tccagttgta ga 32
 <210> 968
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 968
 gaacttgaag taggtgcact gtt 23
 <210> 969
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 969
 gaacttgaag taggtgcact gtt 23

<210> 970

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 970

gaacttgaag taggtgcact gtt

23

<210> 971

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 971

gaacttgaag taggtgcact gtt

23

<210> 972

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 972

tacaaagaaa acacaggtga tct

23

<210> 973

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 973

cggaggaagc agttggtgat ctcggcgg

28

<210> 974
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 974
 caacgcttcc tccg 14
 <210> 975
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 975
 aacgaggcgc acccttcttg ggcattg 26
 <210> 976
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 976
 ttctagacac tgaagatggt tcagttctgt gga 33
 <210> 977
 <211> 19
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 977

catgcccaag aagggtgcg

19

<210> 978

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 978

cggaagaagc agttggtgcg cctcgtaa

29

<210> 979

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 979

caacgcttcc tccg

14

<210> 980

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 980

aacgaggcgc actaattcca ttcaaatca tct

33

<210> 981
 <211> 34
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 981
 catcctggtg agtttgggat tcttgtaatt tata 34
 <210> 982
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 982
 gtaaattccag cagtaaattgc tccag 25
 <210> 983
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 983
 agatgatttt gaatggaatt agtggt 26
 <210> 984
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 984
 cggaagaagc agttggtgcg cctcgtaa 29

<210> 985
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 985
 caacgcttcc tccg 14
 <210> 986
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 986
 cctgtctcgc tgccagttgt gttcttggag 30
 <210> 987
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 987
 ccctgcagaa ggtttccttc ta 22
 <210> 988
 <211> 22
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 988

ccctgcagat ggtttccttc ta

22

<210> 989

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 989

ctccaagaac acaactggca gc

22

<210> 990

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 990

ctccaagaac acaactggca gcga

24

<210> 991

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 991

ctccaagaac acaactggca gcgaga

26

<210> 992

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 992

cggaggaagc agttggcagc gagacagg

28

<210> 993

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 993

caacgcttcc tccg

14

<210> 994

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 994

aacgaggcgc accttggagg cagcaaa

27

<210> 995

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 995

aacgaggcgc accttggagg cagcaa

26

<210> 996

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 996

aaggtttcct tctcagttgt gtta

24

<210> 997

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 997

ctttgctgcc tccaaggtgc g

21

<210> 998

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 998

cggaggaagc agttggtgcg cctcgtaa

29

<210> 999

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 999

caacgcttcc tccg

14

<210> 1000

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1000

cagtcacgtc tctggaggca gcaaagatg

29

<210> 1001

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1001

aagggttcct tctcagttgt gttcta

26

<210> 1002

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1002

catctttgct gcctccagag acg

23

<210> 1003

<211> 29

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1003
 gctactgaga tgaaggagac gtgactgta 29
 <210> 1004
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1004
 cttctctcag tagc 14
 <210> 1005
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1005
 aacgaggcgc accttgagg cagcaaag 28
 <210> 1006
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 1006
 aaggtttcct tctcagttgt gtta 24
 <210> 1007
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1007
 ctttgctgcc tccaaggtgc g 21
 <210> 1008
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1008
 cggaggaagc agttggtgcg cctcgtaa 29
 <210> 1009
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1009
 caacgcttcc tccg 14

<210>	1010	
<211>	32	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1010	
	cgccgagatc accccttttag tttacaaca gt	32
<210>	1011	
<211>	29	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1011	
	gaattggcac tcaaattgtgt tgtcagaga	29
<210>	1012	
<211>	28	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1012	
	actggtgtaa aactaaaggg ggtgatct	28
<210>	1013	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1013	
	cggaggaagc ggttggtgat ctcggcg	27

<210> 1014
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 1014
 caacgcttcc tccg 14
 <210> 1015
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1015
 tgccgcccag atcaccctt tagttttaca acagt 35
 <210> 1016
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1016
 gaattggcac tcaaattgtg tgtcagaga 29
 <210> 1017
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1017

actgttgtaa aactaaaggg ggtg

24

<210> 1018

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1018

actgttgtaa aactaaaggg ggtgat

26

<210> 1019

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1019

actgttgtaa aactaaaggg ggtgatct

28

<210> 1020

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1020

actgttgtaa aactaaaggg ggtgatctcg

30

<210> 1021

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1021

cggaggaagc ggttggtgat ctcggcggca

30

<210> 1022

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 1022

caacgcttcc tccg

14

<210> 1023

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1023

gccgccgaga tcaccccttt agttttacaa cagt

34

<210> 1024

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1024

ccgccgagat cacccttta gttttacaac agt

33

<210> 1025
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1025
 gaattggcac tcaaattgtgt tgtcagaga 29
 <210> 1026
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1026
 actggttgtaa aactaaaggg ggtgat 26
 <210> 1027
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1027
 cggaggaagc gggttggtgat ctcggcggca 30
 <210> 1028
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye

 <400> 1028
 caacgcttcc tccg 14

 <210> 1029
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

 <400> 1029
 aacgaggcgc acccctttag ttttacaaca gt 32

 <210> 1030
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

 <400> 1030
 gaattggcac tcaaattgtgt tgtcagaga 29

 <210> 1031
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

 <400> 1031
 agtaactgtt gtaaaactaa aggggtgcg 29

<210> 1032
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1032
 cggaggaagc agttggtgcg cctcgtaa 29
 <210> 1033
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1033
 caacgcttcc tccg 14
 <210> 1034
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1034
 aacgaggcgc acccctttag ttttacaaca gt 32

<210> 1035

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1035

gaattggcac tcaaattgtgt tgtcagaga

29

<210> 1036

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1036

agtaactgtt gtaaaactaa aggggtgcg

29

<210> 1037

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1037

cggaggaagc agttggtgcg cctcgtaa

29

<210> 1038

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 1038
 caacgcttcc tccg 14
 <210> 1039
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1039
 ccgtcacgcc tccccttttag ttttacaac 29
 <210> 1040
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1040
 gaattggcac tcaaattgtgt tgtcagaga 29
 <210> 1041
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1041
 agttactctg atattgctga tgaaattctc ag 32

<210> 1042
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1042
 gttgtaaaac taaaggggag gcg 23
 <210> 1043
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1043
 cggaagaagc agttggaggc gtgacggt 28
 <210> 1044
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1044
 caacgcttcc tccg 14

<210> 1045
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1045
 cgccgagatc accccttttag ttttacaac 29
 <210> 1046
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1046
 gaattggcac tcaaattgtg tgtcagaga 29
 <210> 1047
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1047
 agttactctg atattgctga tgaaattctc ag 32
 <210> 1048
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1048
 gttgtaaaac taaaggggtg atc 23

<210> 1049
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1049
 cggaagaagc agttggtgat ctgggcgg 28
 <210> 1050
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1050
 caacgcttcc tccg 14
 <210> 1051
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1051
 ccgtcacgcc tcccctttag ttttaca 28
 <210> 1052
 <211> 29
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1052

gaattggcac tcaaattgtgt tgtcagaga

29

<210> 1053

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1053

cagttactct gatattgctg atgaaattct ca

32

<210> 1054

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1054

gttgtaaaac taaaggggag gcg

23

<210> 1055

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1055

cggaagaagc agttggaggc gtgacggt

28

<210> 1056

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 1056

caacgcttcc tccg

14

<210> 1057

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1057

ccgtcacgcc tccccttttag ttttaca

28

<210> 1058

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1058

gaattggcac tcaaattgtgt tgtcagaga

29

<210> 1059
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1059
 cagttactct gatattgctg atgaaattct ca 32
 <210> 1060
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1060
 gttgtaaaac taaaggggag gcg 23
 <210> 1061
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1061
 ccaggaagca gttggaggcg tgacggt 27
 <210> 1062
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 1062
 caacgcttcg tgg 13
 <210> 1063
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1063
 ccgtcacgcc tcccgttagc taagat 26
 <210> 1064
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1064
 cgagggttttc caaggagttg tttta 24
 <210> 1065
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1065
 ccctggatca gatttagaga gc 22

<210> 1066
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1066
 atcttagcta acgggagggcg 20
 <210> 1067
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1067
 cggaagaagc agttggaggc gtgacggt 28
 <210> 1068
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1068
 caacgcttcc tccg 14
 <210> 1069
 <211> 25
 <212> DNA

<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 1069	
ccgtcacgcc tcagttgttt ccggtt	25
<210> 1070	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 1070	
agaggtacaa acgaggtttt ccaaggc	27
<210> 1071	
<211> 29	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 1071	
agctaagatc cctggatcag atttagaga	29
<210> 1072	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 1072	
aacggaaaca actgaggcg	19

<210> 1073
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1073
 ccaggaagca agtggaggcg tgacggg 27
 <210> 1074
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
 <400> 1074
 cactgcttcg tgg 13
 <210> 1075
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1075
 ccgtcacgcc tcccgttagc ta 22

<210>	1076	
<211>	25	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1076	
	caaacgaggt tttccaagga gttga	25
<210>	1077	
<211>	28	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1077	
	agatccctgg atcagattta gagagctc	28
<210>	1078	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1078	
	tagctaacgg aaagaggcg	19
<210>	1079	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1079	
	ccaggaagca agtggaggcg tgacggg	27

<210> 1080
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
 <400> 1080
 cactgcttcg tgg 13
 <210> 1081
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1081
 ccgtcacgcc tcccgttag 19
 <210> 1082
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1082
 agaggtagaa acgaggtttt ccaaggaga 29
 <210> 1083
 <211> 28
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1083

ctaagatccc tggatcagat ttagagag

28

<210> 1084

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1084

ctaacggaaa caagaggcg

19

<210> 1085

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1085

ccaggaagca agtggaggcg tgacggu

27

<210> 1086

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (3)..(3)

<223> The residue at this position is linked to a Z21 quenching group.

<400> 1086

cactgcttcg tgg

13

<210> 1087
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1087
 aacgaggcgc accttaccaa tgcctaagaa aagagtt 37
 <210> 1088
 <211> 36
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1088
 tgcattatTT ttctgtcact ctctcttttc caatta 36
 <210> 1089
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1089
 aactcttttc ttaggcattt tgaaggtgcg 30
 <210> 1090
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1090
 cggaggaagc agttggtgcg cctcgtaa 29

<210> 1091
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 1091
 caacgcttcc tccg 14
 <210> 1092
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1092
 cagtcacgtc tctcttcaaa atgcctaaga aaagagt 37
 <210> 1093
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1093
 tctgcattat ttttctgtca ctctctcttt tccaata 37
 <210> 1094
 <211> 31
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1094

actcttttct taggcatttt gaagagagac g

31

<210> 1095

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1095

gctactgaga tgaaggagac gtgactgta

29

<210> 1096

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye.

<400> 1096

cttctctcag tagc

14

<210> 1097

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1097

aacgaggcgc acccttttgc cagttcc

27

<210> 1098
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1098
 gctctgcagg attttcatgt caccata 27
 <210> 1099
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1099
 gaggaactgg caaaaggggtg cg 22
 <210> 1100
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1100
 gctactgaga tgaaggagac gtgactgta 29
 <210> 1101
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 1101
 cttctctcag tagc 14
 <210> 1102
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1102
 aacgagggcg acccttttgc cagt 24
 <210> 1103
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1103
 gctctgcagg attttcatgt caccata 27
 <210> 1104
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1104
 tcctccagat atccaagaag agactc 26

<210> 1105
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1105
 actggcaaaa ggcgggc 17
 <210> 1106
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1106
 cggaggaaaag cagttggtgc gcctcguuuaa 30
 <210> 1107
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1107
 cggaagaaaag cagttggtgc gcctcguuuaa 30
 <210> 1108
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye

 <400> 1108
 caacgcttcc tccg 14

 <210> 1109
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

 <400> 1109
 gccgcacgcc gccttttgcc agt 23

 <210> 1110
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

 <400> 1110
 gctctgcagg attttcatgt caccata 27

 <210> 1111
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

 <400> 1111
 tcctccagat atccaagaag agactc 26

<210> 1112
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1112
 actggcaaaa ggcgggc 17
 <210> 1113
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1113
 cggaggaagc agttgcggcg tgcggca 27
 <210> 1114
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1114
 caacgcttcc tccg 14

<210>	1115	
<211>	26	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1115	
	aacgaggcgc acccttttgc cagttc	26
<210>	1116	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1116	
	gctctgcagg attttcatgt caccata	27
<210>	1117	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1117	
	ctccagatat ccaagaagag actc	24
<210>	1118	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1118	
	gaactggcaa aagggtgcg	19

<210> 1119
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1119
 cggaggaagc agttggtgcg cctcgtaa 29
 <210> 1120
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1120
 caacgcttcc tccg 14
 <210> 1121
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1121
 ccgtcacgcc tccttgcaa aactgcacc 29

<210> 1122
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1122
 ccgtcacgcc tccttgcaa aactgcacca 30
 <210> 1123
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1123
 ctttatgcac tgacatctaa gttctttagc actca 35
 <210> 1124
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1124
 tggtgcagtt ttgccaagga ggcg 24
 <210> 1125
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1125
 tggtgcagtt ttgccaagga ggcgtg 26

<210> 1126
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1126
 cggaagaagc agttggaggc gtgacggc 28
 <210> 1127
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1127
 caacgcttcc tccg 14
 <210> 1128
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1128
 ccgtcacgcc tccatcttca ctgattcttg g 31

<210> 1129
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1129
 ccgtcacgcc tccatcttca ctgattcttg ga 32
 <210> 1130
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1130
 agtgttgaag tagatttgct tgaagtttca ctgga 35
 <210> 1131
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1131
 gataccacag agaatgaatt tt 22
 <210> 1132
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1132
 tccaagaatc agtgaagatg gaggcg 26

<210> 1133
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1133
 tccaagaatc agtgaagatg gaggcgtg 28
 <210> 1134
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1134
 gaatcagtga agatggaggc g 21
 <210> 1135
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1135
 cggaagaagc agttggaggc gtagcggc 28
 <210> 1136
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 1136
 caacgcttcc tccg 14
 <210> 1137
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1137
 ccgtcacgcc cttggctcaa ttttgct 27
 <210> 1138
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1138
 ccattcaatt cctgaaatta aagttcggat attctcttgg ca 42
 <210> 1139
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1139
 cctgaaatta aagttcggat attctcttgg ca 32

<210> 1140
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1140
 cctgaaatta aagttcggat attctcttgg ca 32
 <210> 1141
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1141
 agcaaaattg agccaaggga ggcg 24
 <210> 1142
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1142
 agcaaaattg agccaaggga ggcgtg 26
 <210> 1143
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1143
 cggaagaagc agttggaggc gtgacggc 28

<210> 1144
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1144
 caacgcttcc tccg . 14
 <210> 1145
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1145
 ccgtcacgcc tccatcttca ctgattcttg 30
 <210> 1146
 <211> 47
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1146
 ttctagcaaa cccattcaat tctgaaatt aaagttcgga tattcta 47

<210> 1147

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1147

cccattcaat tcctgaaatt aaagttcgga tattcta

37

<210> 1148

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1148

cccattcaat tcctgaaatt aaagttcgga tattcta

37

<210> 1149

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1149

ccaagggcca aggaggcgt

19

<210> 1150

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1150

cggaagaagc agttggaggc gtgacggc

28

<210> 1151
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 1151
 caacgcttcc tccg 14
 <210> 1152
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1152
 ccgtcacgcc tccatcttca ctgattc 27
 <210> 1153
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1153
 agtgttgaag tagatttgct tgaagtttca ctgga 35
 <210> 1154
 <211> 23
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1154
ttggatacca cagagaatga att

23

<210> 1155

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1155
cggaagaagc agttggaggc gtgacggt

28

<210> 1156

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3
dye

<400> 1156
caacgcttcc tccg

14

<210> 1157

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1157
ccgtcacgcc tccatcttca ctgatt

26

<210>	1158	
<211>	35	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1158	
	agtgttgaag tagatttgct tgaagtttca ctgga	35
<210>	1159	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1159	
	cttgatacc acagagaatg aatt	24
<210>	1160	
<211>	28	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1160	
	cggaagaagc agttggaggc gtgacggt	28
<210>	1161	
<211>	14	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye

 <400> 1161
 caacgcttcc tccg 14

 <210> 1162
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

 <400> 1162
 ccgtcacgcc tccatcttca ctgattcttg 30

 <210> 1163
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

 <400> 1163
 agtggtgaag tagatttgct tgaagtttca ctgga 35

 <210> 1164
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

 <400> 1164
 ataccacaga gaatgaattt ttttatg 27

<210> 1165
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1165
 tccaagaatc agtgaagatg gaggcgtg 28
 <210> 1166
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1166
 cggaagaagc agttggaggc gtgacggt 28
 <210> 1167
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1167
 caacgcttcc tccg 14

<210> 1168
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1168
 cggaagaagc agttggtgat ctcggcgg 28
 <210> 1169
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1169
 caacgcttcc tccg 14
 <210> 1170
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1170
 cggaagaagc agttggaggc gtagcggt 28

<210> 1171
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4) .. (4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 1171
 caacgcttcc tccg 14
 <210> 1172
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1172
 ccaggaagca agtggaggcg tgacggg 27
 <210> 1173
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (3) .. (3)
 <223> The residue at this position is linked to a Z21 quenching group.
 <400> 1173
 cactgcttcg tgg 13

<210> 1174
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1174
 cggaggaagc agttggtgat ctggcgcg 28
 <210> 1175
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1175
 caacgcttcc tccg 14
 <210> 1176
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1176
 cggaagaagc agttggaggc gtgacggc 28

<210> 1177
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 1177
 caacgcttcc tccg 14
 <210> 1178
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1178
 ccaggaagca agtggtgcgc ctcgttt 27
 <210> 1179
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (3)..(3)
 <223> The residue at this position is linked to a Z21 quenching group.
 <400> 1179
 cactgcttcg tgg 13

<210> 1180

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1180

cggaggaagc agttggtgcg cctcgtaa

29

<210> 1181

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 1181

caacgcttcc tccg

14

<210> 1182

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1182

cggaggaagc ggttggtgat ctcggcggca

30

<210> 1183

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 1183

caacgcttcc tccg

14

<210> 1184

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1184

gctactgaga tgaaggagac gtgactgta

29

<210> 1185

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 1185

cttctctcag tagc

14

<210> 1186
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1186
 ccaggaagca gttggaggcg tgacggt 27
 <210> 1187
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 1187
 caacgcttcg tgg 13
 <210> 1188
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1188
 aggagccact ccattggatg aagc 24

<210> 1189

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1189
atgtacagaa tccccgggta tttatgcaga

30

<210> 1190

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1190
gtggcgatc acagacaatg agag

24

<210> 1191

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1191
cctcctttat attcccaagt ataacactct aa

32

<210> 1192

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1192
aacgaggcgc accacagaca atgagag

27

<210> 1193
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1193
 ctctcattgt ctgtggtgcg 20
 <210> 1194
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1194
 cctcctttat attcccaagt ataacactct aa 32
 <210> 1195
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1195
 agctcaatgc atgtacagaa tccccgg 27
 <210> 1196
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1196
 agctcaatgc atgtacagaa tccccgg 27

<210> 1197
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1197
 aacgaggcgc accacagaca atgagagag 29
 <210> 1198
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1198
 ctctctcatt gtcgtggtg cg 22
 <210> 1199
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1199
 cctcctttat attcccaagt ataacactct aa 32
 <210> 1200
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1200
 ctcaatgcat gtacagaatc cccggtt 27

<210> 1201
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1201
 aacgaggcgc accacagaca atgagagagc t 31
 <210> 1202
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1202
 agctctctca ttgtctgtgg tgcg 24
 <210> 1203
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1203
 cctcctttat attcccaagt ataacactct aa 32
 <210> 1204
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye

 <400> 1204
 caacgcttcc tccg 14

 <210> 1205
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

 <400> 1205
 aacgaggcgc accacagaca atgagagagc 30

 <210> 1206
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

 <400> 1206
 gctctctcat tgtctgtggt gcg 23

 <210> 1207
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

 <400> 1207
 cctcctttat attcccaagt ataacactct aa 32

 <210> 1208
 <211> 14
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (4)..(4)

<223> The residue at this position is linked to a spacer bearing a Cy3 dye

<400> 1208
caacgcttcc tccg

14

<210> 1209

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1209
aacgaggcgc accacagaca atgagaga

28

<210> 1210

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1210
aacgaggcgc accacagaca atgagaga

28

<210> 1211

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1211
tctctcattg tctgtggtgc gc

22

<210> 1212
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1212
 gctcaatgca tgtacagaat ccccggtt 28
 <210> 1213
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1213
 cctcctttat attcccaagt ataacactct aa 32
 <210> 1214
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1214
 aacgaggcgc accacagaca atgaga 26
 <210> 1215
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1215
 tctcattgtc tgtggtgcgc 20

<210> 1216

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1216

cctcctttat attcccaagt ataacactct aa

32

<210> 1217

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1217

gagctcaatg catgtacaga atccccg

27

<210> 1218

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1218

aacgaggcgc acctcttata agagctc

27

<210> 1219

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1219

aacgaggcgc acctcttata agagctc

27

<210> 1220
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1220
 ttgtggagga aattattgag aaatgttgat ta 32
 <210> 1221
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1221
 gagctctgat aagaggtgcg 20
 <210> 1222
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1222
 ccgtcacgcc tcgccccaca 20
 <210> 1223
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1223
 tgtggggcga ggcg 14

<210> 1224

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1224
cagcacaggc tggtgaccat cataaaac

28

<210> 1225

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1225
cuuuuccaau cuuuuuauca cauuc

25

<210> 1226

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1226
cttttccaga ctttttatga cattc

25

<210> 1227

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1227
cttttccaga ctttttatga c

21

<210> 1228
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1228
 ccgtcacgcc tcgccccaca 20
 <210> 1229
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1229
 ccgtcacgcc tcgccccaca 20
 <210> 1230
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1230
 cagcacaggc tggtgaccat cataaaac 28
 <210> 1231
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1231
 cuuuuccaau cuuuuuuga cauuc 25

<210> 1232
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1232
 ccgtcacgcc tcgccccacc 20
 <210> 1233
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1233
 ccgtcacgcc tcgccccacg 20
 <210> 1234
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1234
 ccgtcacgcc tcgccccact 20
 <210> 1235
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1235
 tgtggggcga ggcg 14

<210> 1236
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1236
 cagcacaggc tgttgaccat cataaaac 28
 <210> 1237
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1237
 cuuuuccaau cuuuuuuga cauuc 25
 <210> 1238
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1238
 ccgtcacgcc tgatcataaa agccc 25
 <210> 1239
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1239
 gggcttttat gatcaggcg 19

<210>	1240	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1240	
	cagcacaggc tggtgaccc	19
<210>	1241	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1241	
	cacacttttc catacttttt atg	23
<210>	1242	
<211>	25	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1242	
	aacgaggcgc acccattgga tgaag	25
<210>	1243	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1243	
	cttcatccaa tgggtgcgc	19

<210> 1244
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1244
 gtacagaatc cccggttatt tatgcagta 29
 <210> 1245
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1245
 cccatcttca tttcagag 18
 <210> 1246
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1246
 gtggcgtatc gtgtctaatt tcaag 25
 <210> 1247
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1247
 aatgggtttt tctggttgaa gaagtccttg a 31

<210> 1248
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1248
 aacgaggcgc accgtgtcta atttcaag 28
 <210> 1249
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1249
 aacgaggcgc accgtgtcta atttcaagg 30
 <210> 1250
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1250
 cttgaaatta gacacggtgc g 21
 <210> 1251
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1251
 aatgggtttt tctggttgaa gaagtccttg a 31

<210> 1252

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1252

aacgaggcgc accgtgtcta atttcaag

28

<210> 1253

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1253

cttgaaatta gacacggtgc g

21

<210> 1254

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1254

aatgggtttt tctggttgaa gaagtccttg a

31

<210> 1255

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1255

gggatctgtg tttctttaca aggt

24

<210> 1256

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1256

aacgaggcgc accgtgtcta atttcaag

28

<210> 1257

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1257

cttgaaatta gacacggttc tc

22

<210> 1258

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1258

ggtttttctg gttgaagaag tccttga

27

<210> 1259

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1259

gggatctctg tttct

15

<210> 1260

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1260

aacgaggcgc accgtgtcta atttcaaggg

30

<210> 1261

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1261

cccttgaaat tagacacggt gcg

23

<210> 1262

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1262

aatgggtttt tctggttgaa gaagtccttg a

31

<210> 1263

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 1263
 caacgcttcc tccg 14
 <210> 1264
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1264
 aacgaggcgc accgtgtcta atttcaagg 29
 <210> 1265
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1265
 aacgaggcgc accgtgtcta atttcaagg 29
 <210> 1266
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1266
 ccttgaaatt agacacggtg cgc 23

<210> 1267
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1267
 ccttgaaatt agacacggtg cgc 23
 <210> 1268
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1268
 aatgggtttt tctggttgaa gaagtccttg a 31
 <210> 1269
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1269
 ggatctgtgt ttctttacaa ggtttgaagg ag 32
 <210> 1270
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1270
 aacgaggcgc accgtgtcta atttcaa 27

<210> 1271
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1271
 ttgaaattag acacggtgcg c 21
 <210> 1272
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1272
 aatgggtttt tctggttgaa gaagtccttg a 31
 <210> 1273
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1273
 ggggatctgt gtttctttac aagg 24
 <210> 1274
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1274
 aacgaggcgc accgtgtcta atttca 26

<210>	1275	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1275	
	tgaaattaga cacggtgcgc	20
<210>	1276	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1276	
	ggtttttctg gttgaagaag tccttga	27
<210>	1277	
<211>	17	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1277	
	aggggatctg tgtttct	17
<210>	1278	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1278	
	tggcgtatct gaccctttgg gaat	24

<210> 1279
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1279
 gaagagcata agttggaatc accaccata 29
 <210> 1280
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1280
 atacggttgg tcctctcaag tcta 24
 <210> 1281
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1281
 cccattgat ttcaacatct ttcttgcaac 30
 <210> 1282
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1282
 aacgaggcgc acgcgtgtct aatttc 26

<210> 1283
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1283
 gaaattagac acgcgtgcgc 20
 <210> 1284
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1284
 ggtttttctg gttgaagaag tccttc 26
 <210> 1285
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1285
 ccggggatct gtgtttc 17
 <210> 1286
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1286
 ccgtcacgcc tcgcgtgtct aatttc 26

<210> 1287
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1287
 gaaattagac acgcgaggcg 20
 <210> 1288
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1288
 ggtttttctg gttgaagaag tccttc 26
 <210> 1289
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1289
 ccggggatct gtgtttc 17
 <210> 1290
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1290
 aacgaggcgc agttcatacg ttcc 24

<210>	1291	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1291	
	ggaacgtatg aactgcgc	18
<210>	1292	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1292	
	ccagcacagg gagttgacca	20
<210>	1293	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1293	
	ccacattttt ccatacttt	19
<210>	1294	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1294	
	ccgtcacgcc tggtcatacg ttcc	24

<210>	1295	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1295	
	ggaacgtatg aacaggcg	18
<210>	1296	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1296	
	ccagcacagg gagttgacca	20
<210>	1297	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1297	
	ccacattttt ccatacttt	19
<210>	1298	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1298	
	aacgaggcgc acagttgacc ttca	24

<210> 1299
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1299
 aacgaggcgc acagttgacc ttca 24
 <210> 1300
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1300
 aacgaggcgc acagttgacc ttca 24
 <210> 1301
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1301
 tgaaggtcaa ctgtgcgc 18
 <210> 1302
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1302
 gtgatggcca gcacagggc 19

<210> 1303	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 1303	
tacgttcccc acatttttc	19
<210> 1304	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 1304	
tacgttcccc acatttttc	19
<210> 1305	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 1305	
ccgtcacgcc tcagttgacc ttca	24
<210> 1306	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 1306	
tgaaggtcaa ctgaggcg	18

<210>	1307	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1307	
	gtgatggcca gcacagggc	19
<210>	1308	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1308	
	tacgttcccc acatttttc	19
<210>	1309	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1309	
	aacgaggcgc actcctctca agt	23
<210>	1310	
<211>	17	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1310	
	acttgagagg agtgcgc	17

<210>	1311	
<211>	29	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1311	
	ccattgattt caacatcttt cttgcaaga	29
<210>	1312	
<211>	22	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1312	
	ctaatagcaa ctgggaataa tc	22
<210>	1313	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1313	
	ccgtcacgcc tctcctctca agt	23
<210>	1314	
<211>	17	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1314	
	acttgagagg agaggcg	17

<210> 1315
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1315
 ccattgattt caacatcttt cttgcaaga 29
 <210> 1316
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1316
 ctaatagcaa ctgggaataa tc 22
 <210> 1317
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1317
 aacgaggcgc acagttgacc ttc 23
 <210> 1318
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1318
 tgaaggtcaa ctgtgcgc 18

<210>	1319	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1319	
	gtgatggcca gcacagggc	19
<210>	1320	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1320	
	atacgttccc cacatttttc	20
<210>	1321	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1321	
	tggcgtatct ggattaaatc ttaaaag	27
<210>	1322	
<211>	31	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1322	
	gacttttatt gagagaacga atggatctaa a	31

<210> 1323
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1323
 aacgaggcgc actggattaa atcttaaaag 30
 <210> 1324
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1324
 gactttttatt gagagaacga atggatctaa a 31
 <210> 1325
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1325
 cttttaagat ttaatccagt gcg 23
 <210> 1326
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1326
 aacgaggcgc actggattaa atcttaaaag 30

<210> 1327
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1327
 gactttttatt gagagaacga atggatctaa a 31
 <210> 1328
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1328
 cttttaagat ttaatccagt gcg 23
 <210> 1329
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1329
 cttcttggtg ttttcca 17
 <210> 1330
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1330
 aggagccact catcccttga ct 22

<210> 1331
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1331
 cttagggaaa tcaggctcca cttacggta 29
 <210> 1332
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1332
 aacgaggcgc acctcatccc ttgact 26
 <210> 1333
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1333
 aacgaggcgc acctcatccc ttgact 26
 <210> 1334
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1334
 agtcaaggga tgaggtgcg 19

<210> 1335
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1335
 cttagggaaa tcaggctcca cttacggta 29
 <210> 1336
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1336
 aacgaggcgc acctcatccc ttgac 25
 <210> 1337
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1337
 gtcaagggat gaggtgcgc 19
 <210> 1338
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1338
 cttagggaaa tcaggctcca cttacggta 29

<210> 1339

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1339

tcagccttta gaacaatggg tttttctggt ag

32

<210> 1340

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1340

tcagccttta gaacaatggg tttttctg

28

<210> 1341

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1341

ctcagccttt agaacaatgg gtttttct

28

<210> 1342

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1342

ctcagccttt agaacaatgg gtttttct

28

<210>	1343	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1343	
	aacgaggcgc acctcatccc ttga	24
<210>	1344	
<211>	25	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1344	
	aacgaggcgc acctcatccc ttgac	25
<210>	1345	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1345	
	tcaagggatg aggtgcgc	18
<210>	1346	
<211>	29	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1346	
	cttagggaaa tcaggctcca cttacggta	29

<210> 1347
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1347
 ctcagccttt agaacaatgg gtttttctgt tag 33
 <210> 1348
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1348
 atacggttgg taaagtaatt tgaggt 26
 <210> 1349
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1349
 gaagcccgtc ttcatttcag ggttctatatt c 31
 <210> 1350
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1350
 aacgaggcgc acgtaaagta atttgaggt 29

<210> 1351
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1351
 gaagcccgtc ttcatttcag ggttctattt c 31
 <210> 1352
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1352
 acctcaaatt actttacgtg cg 22
 <210> 1353
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1353
 aacgaggcgc acgtaaagta atttgaggt 29
 <210> 1354
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1354
 gaagcccgtc ttcatttcag ggttctattt c 31

<210>	1355	
<211>	22	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1355	
	acctcaaatt actttacgtg cg	22
<210>	1356	
<211>	15	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1356	
	ctctggtggt ctggg	15
<210>	1357	
<211>	26	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1357	
	ccgtcacgcc tcgtcataaa tacccc	26
<210>	1358	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1358	
	ggggtcttta tgacgaggcg	20

<210> 1359
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1359
 gccagcatag gctgttgaca c 21
 <210> 1360
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1360
 agacttttct atacttttta taacattc 28
 <210> 1361
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1361
 aacgaggcgc acgtcataaa tacccc 26
 <210> 1362
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1362
 aacgaggcgc acgtcataaa tacccc 26

<210> 1363
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1363
 aacgaggcgc acgtcataaa tacccc 26
 <210> 1364
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1364
 ggggtattta tgacgtgcgc 20
 <210> 1365
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1365
 gccagcatag gctgttgaca c 21
 <210> 1366
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1366
 agacttttct atacttttta taacattc 28

<210> 1367
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1367
 ccgtcacgcc tcgattaaat cttaaaagct t. 31
 <210> 1368
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1368
 aagcttttaa gatttaatcg. aggcg 25
 <210> 1369
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1369
 gacttttatt gagagaacga atggatctaa tgc 33
 <210> 1370
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1370
 cttggtgttt tccacaaag 19

<210> 1371
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1371
 aacgagggcgc acgattaaat cttaaaagct t 31
 <210> 1372
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1372
 aagcttttaa gatttaatcg tgcgc 25
 <210> 1373
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1373
 gacttttatt gagagaacga atggatctaa tgc 33
 <210> 1374
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1374
 cttggtgttt tccacaaag 19

<210> 1375
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1375
 ccgtcacgcc tgtcatccct tg 22
 <210> 1376
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1376
 caagggatgc acggcg 16
 <210> 1377
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1377
 ggaaatcagg ctccacttac ggtca 25
 <210> 1378
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1378
 actcagcctt tagaacaatg 20

<210> 1379
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1379
 ccgtcacgcc tctaaagtaa tttgaggtc 29
 <210> 1380
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1380
 gacctcaaat tactttagag gcg 23
 <210> 1381
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1381
 cgtcttcatt tcagggttct atttga 26
 <210> 1382
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1382
 tctggtgttc tggg 14

<210> 1383

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1383

aacgagggcgc actaaagtaa tttgaggtc

29

<210> 1384

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1384

gacctcaaag gacttttagtg cgc

23

<210> 1385

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1385

cgtcttcatt tcagggttct atttga

26

<210> 1386

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1386

tctggtgttc tggg

14

<210> 1387
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1387
 tggcgtatct aggctttgct tcc 23
 <210> 1388
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1388
 ttcatgtagt cagggtcata gacaattaag a 31
 <210> 1389
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1389
 aacgaggcgc actaggcttt gcttcc 26
 <210> 1390
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1390
 ggaagcaaag cctagtgcg 19

<210> 1391
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1391
 ggaagcaaag cctagtgcgc 20
 <210> 1392
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1392
 ttcattgtagt cagggtcata gacaattaag a 31
 <210> 1393
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1393
 aacgaggcgc actaggcttt gcttccc 27
 <210> 1394
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1394
 gggaagcaaa gcctagtgcg c 21

<210> 1395
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1395
 ttcattgtatg cagggtcata gacaattaag a 31
 <210> 1396
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1396
 aacgaggcgc actaggcttt gcttc 25
 <210> 1397
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1397
 gaagcaaagc ctagtgcg 19
 <210> 1398
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1398
 cccagaacca tcgaggaaag gc 22

<210> 1399
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1399
 ttcatgtagt cagggtcata gacaattaag a 31
 <210> 1400
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1400
 aacgaggcgc actaggcttt gctt 24
 <210> 1401
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1401
 aagcaaagcc tagtgcg 18
 <210> 1402
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1402
 ttcatgtagt cagggtcata gacaattaag a 31

<210>	1403	
<211>	22	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1403	
	ccccagaacc atcgaggaaa gg	22
<210>	1404	
<211>	22	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1404	
	ccccagaacc atcgaggaaa gg	22
<210>	1405	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1405	
	aacgaggcgc actaggcttt gct	23
<210>	1406	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1406	
	aacgaggcgc actaggcttt gct	23

<210>	1407	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1407	
	aacgaggcgc actaggcttt gct	23
<210>	1408	
<211>	17	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1408	
	agcaaagcct agtgcg	17
<210>	1409	
<211>	17	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1409	
	agcaaagcct agtgcg	17
<210>	1410	
<211>	31	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1410	
	ttcatgtagt cagggtcata gacaattaag a	31

<210> 1411
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1411
 tccccagaac catcgaggaa agg 23
 <210> 1412
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1412
 tccccagaac catcgaggaa agg 23
 <210> 1413
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1413
 atacggttg tcttgacctg cc 22
 <210> 1414
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1414
 aggagatatg ttgaaagatt tctatagagg ac 32

<210>	1415	
<211>	25	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1415	
	aacgaggcgc acgtcttgac ctgcc	25
<210>	1416	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1416	
	ggcaggtcaa gacgtgcg	18
<210>	1417	
<211>	32	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1417	
	aggagatatg ttgaaagatt tctatagagg ac	32
<210>	1418	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1418	
	aacgaggcgc acgtcttgac ctgc	24

<210> 1419
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1419
 ggcaggtcaa gacgtgcg 18
 <210> 1420
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1420
 aggagatag ttgaaagatt tctatagagg ac 32
 <210> 1421
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1421
 tggcgtatct tagatggagt aagga 25
 <210> 1422
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1422
 attcctcata attcaaaagg gacttagtag gt 32

<210> 1423
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1423
 aacgaggcgc acttagatgg agtaagga 28
 <210> 1424
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1424
 tccttactcc atctaagtgc g 21
 <210> 1425
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1425
 aacgaggcgc actggatacc cttggg 26
 <210> 1426
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1426
 cccaagggta tccagtgcgc 20

<210> 1427
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1427
 ggtggagacc ataaatggag agtgtgacta 30
 <210> 1428
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1428
 aacgaggcgc acaggtgtct ggagtaaaag 30
 <210> 1429
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1429
 cttttactcc agacacctgt gcgc 24
 <210> 1430
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1430
 gtccacgcac aagctgggac 20

<210>	1431	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1431	
	aacgaggcgc acagaaggcc cctt	24
<210>	1432	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1432	
	aaggggcctt ctgtgcgc	18
<210>	1433	
<211>	31	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1433	
	ccttgaacag caccagaaat agactgagca c	31
<210>	1434	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1434	
	ggaagaaccc agagacacca tcc	23

<210> 1435

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1435

ccgtcacgcc tcagaaggcc cctt

24

<210> 1436

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1436

aaggggcctt ctgaggcg

18

<210> 1437

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1437

ccttgaacag caccagaaat agactgagca c

31

<210> 1438

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1438

aacgaggcgc acagaaggcc ccttg

25

<210> 1439
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1439
 caaggggcct tctgtgcgc 19
 <210> 1440
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1440
 ccttgaacag caccagaaat agactgagca c 31
 <210> 1441
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1441
 aacgaggcgc acagaaggcc ccttgg 26
 <210> 1442
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1442
 aacgaggcgc acagaaggcc cctt 24

<210> 1443
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1443
 aacgaggcgc acagaaggcc cctt 24
 <210> 1444
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1444
 ccaaggggcc ttctgtgcgc 20
 <210> 1445
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1445
 aaggggcctt ctgtgcgc 18
 <210> 1446
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1446
 ccttgaacag caccagaaat agactgagca c 31

<210> 1447
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1447
 aacgaggcgc acttgacaga gtccgc 26
 <210> 1448
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1448
 gcggactctg tcaagtgcgc 20
 <210> 1449
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1449
 gcttctccca tttgtctagc attataa 27
 <210> 1450
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1450
 aacgaggcgc acttgacaga gtccg 25

<210>	1451	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1451	
	cggactctgt caagtgcgc	19
<210>	1452	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1452	
	gcttctccca tttgtctagc attataa	27
<210>	1453	
<211>	29	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1453	
	ccatgatttt gacatagggt ttgaggatg	29
<210>	1454	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	1454	
	aacgaggcgc acttgacaga gtcc	24

<210> 1455
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1455
 aacgaggcgc acttgacaga gtcc 24
 <210> 1456
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1456
 aacgaggcgc acttgacaga gtcc 24
 <210> 1457
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1457
 ggactctgtc aagtgcgc 18
 <210> 1458
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 1458
 ggactctgtc aagtgcgc 18